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Human Nucleic Acid Sequences from Ovarian Tumor Tissue

The invention relates to human nucleic acid sequences from ovarian tumor tissue, which code for gene products or parts thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main cancer causes of death in women is ovarian cancer, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which play a role as candidate genes in ovarian cancer, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a part thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273,
 - b) an allelic variation of the nucleic acid sequences named under a)
- or
- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which are expressed elevated in ovarian tumor tissue.

The invention also relates to nucleic acid sequences Seq. ID Nos. 27, 32, 42, 46, 67, 76, 78, 80, 85, 88, 90, 108, and 112, which are expressed elevated in breast tumor tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R , trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as *E. coli* or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides according to the sequence protocols Seq. ID Nos. 124-257 and 274-307.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID Nos. 124-257 and 274-307 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The invention also relates to phage-display phages, which are directed against a polypeptide or a fragment and which are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273 according to the invention.

The polypeptides of sequences Seq. ID Nos. 124-257 and 274-305 according to the invention can also be used as tools for finding active ingredients against ovarian cancer, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-123 and 258-273 for expression of polypeptides, which can be used as tools for finding active ingredients against ovarian cancer.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 124-257 and 274-305 as pharmaceutical agents in the gene therapy for treatment of ovarian cancer or for the production of a pharmaceutical agent for treatment of ovarian cancer.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 124-257 and 274-305.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID Nos. 1-123 and 258-273, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-123 and 258-273 for use as vehicles for gene transfer.

Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes).

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus).

Singleton = A contig that contains only one sequence.

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins.

N = selectively the nucleotide A, T, G or C.

X = selectively one of the 20 naturally occurring amino acids.

Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

Figure 3 shows the in-silico subtraction of gene expression in various tissues

Figure 4a shows the determination of tissue-specific expression via electronic Northern

Figure 4b shows the electronic Northern

Figure 5 shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for tumor-related candidate genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the ovarian tumor tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2**Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1. Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) *J. Mol. Biol.* 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) *Nucleic Acids Research* 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) *Proc. Natl. Acad. Sci. USA* 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 68 was found which occurs 6.08 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 68

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0141	0.0244	0.5758	1.7366
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0136	0.0226	0.6038	1.6562
Gastrointestinal	0.0211	0.0185	1.1390	0.8780
Brain	0.0126	0.0082	1.5299	0.6536
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0110	0.0847	0.1300	7.6946
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0233	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0143	0.4355	2.2964
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0054	0.0060	0.7930	1.2610
Kidney	0.0066	0.0055	1.1966	0.8357
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0153	0.0043	3.5827	0.2791
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0076	0.0136	0.5611	1.7821
Uterus-myometrium	0.0153	0.0000	undef	0.0000
Uterus-general	0.0384			
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0000			
Testicular hyperplasia	0.0235			
Seminal vesicle	0.0147			
Sensory organs	0.0426			
White blood cells				
Cervix				

	FETUS % frequency
Development	0.0139
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0178
Lung	0.0108
Suprarenal gland	0.0254
Kidney	0.0062
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0000

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0244
Hematopoietic	0.0057
Skin-muscle	0.0259
Testicles	0.0000
Lung	0.0040
Nerves	0.0479
Prostate	0.0000
Sensory Organs	0.0083
Uterus_n	

2.1.2

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 86 was found which occurs 7.82 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 86

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0128	0.9153	1.0926
Breast	0.0090	0.0169	0.5293	1.8893
Small intestine	0.0092	0.0331	0.2781	3.5964
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0204	0.0426	0.4795	2.0856
Gastrointestinal	0.0211	0.0185	1.1390	0.8780
Brain	0.0274	0.0195	1.4020	0.7133
Hematopoietic	0.0107	0.1136	0.0941	10.6267
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0307	0.0137	2.2358	0.4473
Testicles	0.0115	0.0819	0.1406	7.1142
Lung	0.0104	0.0286	0.3629	2.7557
Stomach-esophagus	0.0290	0.0153	1.8908	0.5289
Muscle-skeleton	0.0188	0.0300	0.6282	1.5918
Kidney	0.0163	0.0342	0.4758	2.1016
Pancreas	0.0132	0.0110	1.1966	0.8357
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0174	0.0234	0.7445	1.3433
Uterus-endometrium	0.0270	0.5277	0.0512	19.5264
Uterus-myometrium	0.0229	0.0408	0.5611	1.7821
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0297			
Seminal vesicle	0.0353			
Sensory organs	0.0095			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development		0.0000
Gastrointestinal	0.0696	0.0000
Brain	0.0167	0.0000
Hematopoietic	0.0626	0.0245
Skin	0.0079	0.0000
Hepatic	0.0000	0.0000
Heart-blood vessels	0.0285	0.0000
Lung	0.0072	0.0000
Suprarenal gland	0.0000	0.0000
Kidney	0.0062	0.0097
Placenta	0.0303	0.0000
Prostate	0.0997	0.0000
Sensory organs	0.0126	0.0155
Breast		0.0000
Ovary_n		0.0000
Ovary_t		0.0000
Endocrine tissue		0.0000
Fetal		0.0000
Gastrointestinal		0.0000
Hematopoietic		0.0000
Skin-muscle		0.0000
Testicles		0.0000
Lung		0.0010
Nerves		0.0000
Prostate		0.0000
Sensory Organs		0.0000
Uterus_n		0.0000

2.1.3

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 114 was found which occurs 6.94 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 114

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0117	0.0026	4.5763	0.2185
Small intestine	0.0026	0.0075	0.3403	2.9389
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0208	0.1439	6.9489
Gastrointestinal	0.0085	0.0025	3.3962	0.2944
Brain	0.0057	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0083	0.0102	0.8129	1.2302
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0136	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0065	0.0064	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0305	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032	0.0089	0.0445	
Prostate hyperplasia	0.0089	0.0445	0.0000	
Seminal vesicle	0.0045	0.0000	0.0000	
Sensory organs	0.0213	0.0000	0.0000	
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0062
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.1418
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0154
Lung	0.0000
Nerves	0.0000
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0000

In an analogous procedure, the following Northerns were also found:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0179	0.0075	2.3818	0.4198
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0120	0.0364	0.3289	3.0402
Endocrine tissue	0.0119	0.0100	1.1887	0.9413
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0059	0.0103	0.5760	1.7362
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0095	0.0129	0.7353	1.3600
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0000	0.0351	0.0000	undef
Lung	0.0052	0.0164	0.3175	3.1494
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0061			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0136
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0070
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0032
Suprarenal gland	Testicles	0.0154
Kidney	Lung	0.0164
Placenta	Nerves	0.0205
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0083
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 2

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0026	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0182	0.0000	undef
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency
Development	
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0171
Skin-muscle	0.0194
Testicles	0.0082
Lung	0.0020
Nerves	0.0137
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 3

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0026	4.5763	0.2185
Breast	0.0064	0.0019	3.4026	0.2939
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0193	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0044	0.0000	undef	0.0000
Prostate	0.0135	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0051	0.1908	0.0267	37.4714
Uterus-general	0.0096			
Breast hyperplasia	0.0178			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0106			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0064
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0065
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 4

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000 undef	
Small intestine	0.0051	0.0000	undef 0.0000	
Ovary	0.0000	0.0000	undef undef	
Endocrine tissue	0.0000	0.0572	0.0000 undef	
Gastrointestinal	0.0034	0.0075	0.4528 2.2083	
Brain	0.0019	0.0093	0.2071 4.8289	
Hematopoietic	0.0022	0.0021	1.0799 0.9260	
Skin	0.0013	0.0379	0.0353 28.3379	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0053	0.0000	0.0000 undef	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0104	0.0041	2.5402 0.3937	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0017	0.0000	undef 0.0000	
Kidney	0.0027	0.0000	undef 0.0000	
Pancreas	0.0083	0.0000	undef 0.0000	
Penis	0.0030	0.0000	undef 0.0000	
Prostate	0.0022	0.0000	undef 0.0000	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0051	0.0000	undef undef	
Uterus-general	0.0128	0.0000	undef 0.0000	
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0106			
Cervix				

	FETUS % frequency
Development	
Gastrointestinal	0.0278
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0093
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0060
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0208
Uterus_n	

Electronic Northern for SEQ. ID NO.: 5

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0012
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 6

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0141	0.0075	1.8715	0.5343
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0120	0.0390	0.3070	3.2573
Endocrine tissue	0.0290	0.0376	0.7698	1.2990
Gastrointestinal	0.0211	0.0324	0.6508	1.5365
Brain	0.0126	0.0144	0.8742	1.1439
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0218	0.0204	1.0669	0.9373
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0137	0.0000	undef	0.0000
Kidney	0.0190	0.0205	0.9252	1.0808
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0109	0.0106	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0408	0.3741	2.6732
Uterus-general	0.0306	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0217			
Cervix	0.0319			

	FETUS % frequency
Development	
Gastrointestinal	0.0557
Brain	0.0167
Hematopoietic	0.0063
Skin	0.0079
Hepatic	0.0000
Heart-blood vessels	0.0213
Lung	0.0213
Suprarenal gland	0.0181
Kidney	0.0254
Placenta	0.0185
Prostate	0.0121
Sensory organs	0.0000
	0.0251

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0476
Ovary_n	0.3190
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0151
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0309
Lung	0.0082
Nerves	0.0010
Prostate	0.0000
Sensory Organs	0.0310
Uterus_n	0.0458

Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0077	0.0000 undef
Breast	0.0026	0.0113	0.2268 4.4083
Small intestine	0.0031	0.0331	0.0927 10.7893
Ovary	0.0000	0.0182	0.0000 undef
Endocrine tissue	0.0051	0.0050	1.0189 0.9815
Gastrointestinal	0.0057	0.0139	0.4142 2.4145
Brain	0.0030	0.0010	2.8798 0.3472
Hematopoietic	0.0027	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0062	0.0123	0.5080 1.9684
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0163	0.0205	0.7930 1.2610
Kidney	0.0017	0.0055	0.2991 3.3428
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0000	0.0021	0.0000 undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0064	0.0000	undef undef
Uterus-general	0.0030	0.0000	
Breast hyperplasia	0.0000	0.0000	
Prostate hyperplasia	0.0000	0.0000	
Seminal vesicle	0.0000	0.0000	
Sensory organs	0.0106	0.0000	
White blood cells			
Cervix			

	FETUS % frequency
Development	
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0072
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0120
Nerves	0.0205
Prostate	0.0077
Sensory Organs	0.0042
Uterus_n	

Electronic Northern for SEQ. ID NO.: 8

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0064	0.0038	1.7013 0.5878
Small intestine	0.0031	0.0000	undef 0.0000
Ovary	0.0000	0.0156	0.0000 undef
Endocrine tissue	0.0068	0.0125	0.5434 1.8403
Gastrointestinal	0.0000	0.0046	0.0000 undef
Brain	0.0037	0.0000	undef 0.0000
Hematopoietic	0.0027	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0042	0.0137	0.3084 3.2426
Testicles	0.0058	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0060	0.0000 undef
Muscle-skeleton	0.0054	0.0068	0.7930 1.2610
Kidney	0.0050	0.0000	undef 0.0000
Pancreas	0.0120	0.0000	undef 0.0000
Penis	0.0022	0.0000	undef 0.0000
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0068	0.0000 undef
Uterus-myometrium	0.0000	0.0000	undef undef
Uterus-general	0.0089		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0118		
Seminal vesicle	0.0026		
Sensory organs	0.0000		
White blood cells			
Cervix			

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0111
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lung	0.0020
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0333
Uterus_n	

Electronic Northern for SEQ. ID NO.: 9

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0034	0.0201	0.1698	5.8889
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0081	0.0072	1.1314	0.8839
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0010	0.0020	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0054	0.0000	undef	0.0000
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0065	0.0043	1.5354	0.6513
Prostate	0.0068	0.1583	0.0427	23.4317
Uterus-endometrium	0.0152	0.0000	undef	0.0000
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0149			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0093
Gastrointestinal	0.0000
Hematopoietic	0.0032
Skin-muscle	0.0309
Testicles	0.0000
Lung	0.0100
Nerves	0.0000
Prostate	0.0077
Sensory Organs	0.0250
Uterus_n	

Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0013	0.0019	0.6805 1.4694
Small intestine	0.0031	0.0000	undef 0.0000
Ovary	0.0000	0.0182	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0000	0.0000	undef undef
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0013	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0011	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0051	0.0000	undef undef
Uterus-myometrium	0.0000		undef 0.0000
Uterus-general	0.0000		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0009		
Sensory organs	0.0000		
White blood cells			
Cervix			

FETUS % frequency	
Development	
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0125
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0026	6.1018	0.1639
Breast	0.0102	0.0038	2.7221	0.3674
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0170	0.0201	0.8491	1.1778
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0126	0.0072	1.7485	0.5719
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0093	0.0061	1.5241	0.6561
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0137	0.0180	0.7615	1.3133
Kidney	0.0054	0.0479	0.1133	8.8268
Pancreas	0.0083	0.0055	1.4957	0.6686
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0021	4.0945	0.2442
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.0068	5.6113	0.1782
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0095			
White blood cells	0.0000			
Cervix				

	FETUS % frequency
Development	
Gastrointestinal	0.0139
Brain	0.0083
Hematopoietic	0.0063
Skin	0.0063
Hepatic	0.0118
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0107
Kidney	0.0072
Placenta	0.0000
Prostate	0.0247
Sensory organs	0.0182
	0.0249
	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES

	% frequency
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0082
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0259
Testicles	0.0154
Lung	0.0082
Nerves	0.0040
Prostate	0.0205
Sensory Organs	0.0000
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 13

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0026	0.0019	1.3611 0.7347
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0156	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0000	0.0000	undef undef
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0011	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0010	0.0020	0.5080 1.9684
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0055	0.0000 undef
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0044	0.0021	2.0473 0.4885
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0000	0.0000	undef undef
Uterus-general	0.0000		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0235		
Seminal vesicle	0.0000		
Sensory organs	0.0000		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0068
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0012
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0077
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0020
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0042
	Uterus_n

Electronic Northern for SEQ. ID NO.: 15

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0086	0.0120	0.7139	1.4008
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0087	0.0064	1.3648	0.7327
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0059			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0035			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0072
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0061
Placenta	0.0000
Prostate	0.0000
Sensory organs	
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0017
Fetal	0.0000
Gastrointestinal	0.0057
Hematopoietic	0.0032
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0010
Nerves	0.0137
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0117	0.0179	0.6538 1.5296
Breast	0.0307	0.0226	1.3611 0.7347
Small intestine	0.0215	0.0000	undef 0.0000
Ovary	0.0090	0.0338	0.2657 3.7640
Endocrine tissue	0.0034	0.0050	0.6792 1.4722
Gastrointestinal	0.0192	0.0185	1.0354 0.9658
Brain	0.0074	0.0133	0.5538 1.8057
Hematopoietic	0.0067	0.0000	undef 0.0000
Skin	0.0257	0.0000	undef 0.0000
Hepatic	0.0048	0.0065	0.7353 1.3600
Heart	0.0148	0.0137	1.0794 0.9265
Testicles	0.0115	0.0000	undef 0.0000
Lung	0.0353	0.0164	2.1591 0.4631
Stomach-esophagus	0.0387	0.0077	5.0421 0.1983
Muscle-skeleton	0.0154	0.0120	1.2850 0.7782
Kidney	0.0163	0.0274	0.5948 1.6813
Pancreas	0.0198	0.0166	1.1966 0.8357
Penis	0.0090	0.0267	0.3369 2.9678
Prostate	0.0196	0.0064	3.0709 0.3256
Uterus-endometrium	0.0338	0.0000	undef 0.0000
Uterus-myometrium	0.0229	0.0000	undef 0.0000
Uterus-general	0.0000	0.0000	undef undef
Breast hyperplasia	0.0353		
Prostate hyperplasia	0.0178		
Seminal vesicle	0.0182		
Sensory organs	0.0426		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0136
Gastrointestinal	Ovary_n 0.1595
Brain	Ovary_t 0.0051
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0041
Hepatic	Gastrointestinal 0.0244
Heart-blood vessels	Hematopoietic 0.0114
Lung	Skin-muscle 0.0130
Suprarenal gland	Testicles 0.0077
Kidney	Lung 0.0164
Placenta	Nerves 0.0110
Prostate	Prostate 0.0274
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0458

Electronic Northern for SEQ. ID NO.: 18

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0000	0.0125	0.0000	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0044	0.0021	2.1599	0.4630
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0104	0.0041	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0083	0.0000	undef	0.0000
Kidney	0.0060	0.0000	undef	0.0000
Pancreas	0.0022	0.0021	1.0236	0.9769
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0096			
Uterus-general	0.0000			
Breast hyperplasia	0.0118			
Prostate hyperplasia	0.0017			
Seminal vesicle	0.0319			
Sensory organs				
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0203
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0128
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0259
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0164
Placenta	Nerves	0.0100
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0333
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 19

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0000	0.0019	0.0000 undef
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0130	0.0000 undef
Endocrine tissue	0.0038	0.0000	undef 0.0000
Gastrointestinal	0.0007	0.0000	undef 0.0000
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0020	0.0000 undef
Lung	0.0000	0.0077	0.0000 undef
Stomach-esophagus	0.0051	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0022	0.0000	undef 0.0000
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000		undef undef
Uterus-myometrium	0.0000		
Uterus-general	0.0000		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs			
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0051
Hematopoietic	Endocrine tissue 0.0245
Skin	Fetal 0.0029
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0065
Lung	Skin-muscle 0.0077
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0020
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0042
	Uterus_n

Electronic Northern for SEQ. ID NO.: 20

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0039	0.0000	undef 0.0000
Breast	0.0013	0.0019	0.6805 1.4694
Small intestine	0.0061	0.0000	undef 0.0000
Ovary	0.0000	0.0208	0.0000 undef
Endocrine tissue	0.0051	0.0000	undef 0.0000
Gastrointestinal	0.0038	0.0000	undef 0.0000
Brain	0.0030	0.0021	1.4399 0.6945
Hematopoietic	0.0053	0.0000	undef 0.0000
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0032	0.0137	0.2313 4.3235
Testicles	0.0000	0.0000	undef undef
Lung	0.0073	0.0020	3.5562 0.2812
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0050	0.0000	undef undef
Kidney	0.0000	0.0000	undef 0.0000
Pancreas	0.0050	0.0021	undef undef
Penis	0.0044	0.0000	2.0473 0.4885
Prostate	0.0068	0.0000	undef 0.0000
Uterus-endometrium	0.0076	0.0000	undef 0.0000
Uterus-myometrium	0.0000	0.0000	undef undef
Uterus-general	0.0032	0.0000	
Breast hyperplasia	0.0030	0.0000	
Prostate hyperplasia	0.0000	0.0000	
Seminal vesicle	0.0061	0.0000	
Sensory organs	0.0000	0.0000	
White blood cells	0.0000	0.0000	
Cervix	0.0000	0.0000	

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0029
Hepatic	Gastrointestinal 0.0171
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0068
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 21

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0000	0.0000	undef undef
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0130	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0015	0.0000	undef 0.0000
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0000		
Uterus-general	0.0000		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs			
White blood cells			
Cervix			

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0020
Nerves	0.0000
Prostate	0.0155
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 22

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0068	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 23

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0051	0.0000 undef
Breast	0.0051	0.0019	2.7221 0.3674
Small intestine	0.0031	0.0331	0.0927 10.7893
Ovary	0.0000	0.0182	0.0000 undef
Endocrine tissue	0.0034	0.0100	0.3396 2.9444
Gastrointestinal	0.0096	0.0093	1.0354 0.9658
Brain	0.0059	0.0021	2.8798 0.3472
Hematopoietic	0.0000	0.0379	0.0000 undef
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0129	0.0000 undef
Heart	0.0011	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0042	0.0061	0.6774 1.4763
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0027	0.0137	0.1983 5.0439
Pancreas	0.0099	0.0055	1.7949 0.5571
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0000	0.0021	0.0000 undef
Uterus-endometrium	0.0076	0.0000	undef undef
Uterus-myometrium	0.0000	0.0000	undef 0.0000
Uterus-general	0.0064	0.0059	0.0000 undef
Breast hyperplasia	0.0000	0.0000	undef undef
Prostate hyperplasia	0.0000	0.0017	undef 0.0000
Seminal vesicle	0.0000	0.0000	undef undef
Sensory organs	0.0000	0.0000	undef undef
White blood cells	0.0000	0.0000	undef undef
Cervix	0.0000	0.0000	undef undef

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0139	Breast 0.0000
Gastrointestinal	0.0000	Ovary_n 0.0000
Brain	0.0000	Ovary_t 0.0000
Hematopoietic	0.0000	Endocrine tissue 0.0000
Skin	0.0000	Fetal 0.0000
Hepatic	0.0000	Gastrointestinal 0.0000
Heart-blood vessels	0.0000	Hematopoietic 0.0000
Lung	0.0000	Skin-muscle 0.0000
Suprarenal gland	0.0000	Testicles 0.0000
Kidney	0.0062	Lung 0.0000
Placenta	0.0000	Nerves 0.0068
Prostate	0.0249	Prostate 0.0000
Sensory organs	0.0000	Sensory Organs 0.0000
		Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 24

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0153	0.0226	0.6792	1.4722
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0081	0.0092	0.8800	1.1364
Hematopoietic	0.0067	0.0379	0.1764	5.6676
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0102	0.8129	1.2302
Lung	0.0083	0.0153	0.0000	undef
Stomach-esophagus	0.0103	0.0180	0.5711	1.7510
Muscle-skeleton	0.0081	0.0068	1.1896	0.8406
Kidney	0.0033	0.0000	undef	0.0000
Pancreas	0.0329	0.0000	undef	0.0000
Penis	0.0153	0.0064	2.3885	0.4187
Prostate	0.0135	0.1055	0.1280	7.8106
Uterus-endometrium	0.0305	0.0136	2.2445	0.4455
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0064			
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0069			
White blood cells	0.0106			
Cervix				

	FETUS % frequency
Development	0.0139
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0121
Placenta	0.0249
Prostate	0.0000
Sensory organs	

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.0203
Endocrine tissue	0.0245
Fetal	0.0099
Gastrointestinal	0.0122
Hematopoietic	0.0171
Skin-muscle	0.0097
Testicles	0.0000
Lung	0.0246
Nerves	0.0060
Prostate	0.0205
Sensory Organs	0.0387
Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 25

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0204	0.1907 5.2444
Breast	0.0141	0.0263	0.5347 1.8702
Small intestine	0.0061	0.0000	undef 0.0000
Ovary	0.0090	0.0312	0.2878 3.4745
Endocrine tissue	0.0136	0.0150	0.9057 1.1042
Gastrointestinal	0.0192	0.0185	1.0354 0.9658
Brain	0.0222	0.0113	1.9635 0.5093
Hematopoietic	0.0094	0.0000	undef 0.0000
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0048	0.0129	0.3676 2.7200
Heart	0.0148	0.0000	undef 0.0000
Testicles	0.0000	0.0234	0.0000 undef
Lung	0.0135	0.0123	1.1007 0.9085
Stomach-esophagus	0.0097	0.0153	0.6303 1.5866
Muscle-skeleton	0.0188	0.0300	0.6282 1.5918
Kidney	0.0163	0.0205	0.7930 1.2610
Pancreas	0.0083	0.0221	0.3739 2.6743
Penis	0.0090	0.0267	0.3369 2.9678
Prostate	0.0068	0.0043	2.5591 0.3908
Uterus-endometrium	0.0076	0.0204	0.3741 2.6732
Uterus-myometrium	0.0102	0.0954	0.1067 9.3678
Uterus-general	0.0032		
Breast hyperplasia	0.0119		
Prostate hyperplasia	0.0089		
Seminal vesicle	0.0235		
Sensory organs	0.0087		
White blood cells	0.0000		
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.1595
Hematopoietic	Endocrine tissue	0.0203
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0058
Heart-blood vessels	Hematopoietic	0.0488
Lung	Skin-muscle	0.0114
Suprarenal gland	Testicles	0.0032
Kidney	Lung	0.0154
Placenta	Nerves	0.0164
Prostate	Prostate	0.0060
Sensory organs	Sensory Organs	0.0068
	Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 26

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0234	0.0204	1.1441 0.8741
Breast	0.0192	0.0470	0.4083 2.4491
Small intestine	0.0184	0.0000	undef 0.0000
Ovary	0.0090	0.0546	0.1645 6.0803
Endocrine tissue	0.0204	0.0075	2.7170 0.3681
Gastrointestinal	0.0268	0.0416	0.6443 1.5522
Brain	0.0037	0.0154	0.2400 4.1669
Hematopoietic	0.0147	0.0000	undef 0.0000
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0476	0.0259	1.8382 0.5440
Heart	0.0095	0.0412	0.2313 4.3235
Testicles	0.0000	0.0000	undef undef
Lung	0.0166	0.0184	0.9032 1.1072
Stomach-esophagus	0.0387	0.0460	0.8404 1.1900
Muscle-skeleton	0.0543	0.0411	1.3217 0.7566
Kidney	0.0363	0.0110	3.2906 0.3039
Pancreas	0.0060	0.0267	0.2246 4.4517
Penis	0.0218	0.0128	1.7060 0.5862
Prostate	0.0338	0.0000	undef 0.0000
Uterus-endometrium	0.0000	0.0136	0.0000 undef
Uterus-myometrium	0.0051	0.0954	0.0534 18.7357
Uterus-general	0.0352		
Breast hyperplasia	0.0535		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0235		
Sensory organs	0.0078		
White blood cells	0.0106		
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0204
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0101
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0017
Hepatic	Gastrointestinal 0.0244
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0040
Placenta	Nerves 0.0137
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0083
	Uterus_n

Electronic Northern for SEQ. ID NO.: 27

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0026	0.0000 undef
Breast	0.0013	0.0038	0.3403 2.9389
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0130	0.0000 undef
Endocrine tissue	0.0034	0.0000	undef 0.0000
Gastrointestinal	0.0038	0.0000	undef 0.0000
Brain	0.0074	0.0051	1.4399 0.6945
Hematopoietic	0.0027	0.0379	0.0706 14.1689
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0032	0.0000	undef 0.0000
Testicles	0.0058	0.0000	undef 0.0000
Lung	0.0021	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0054	0.0068	0.7930 1.2610
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0090	0.0000	undef 0.0000
Penis	0.0022	0.0128	0.1706 5.8615
Prostate	0.0000	0.0068	0.0000 undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0000		
Uterus-general	0.0000		
Breast hyperplasia	0.0089		
Prostate hyperplasia	0.0235		
Seminal vesicle	0.0017		
Sensory organs	0.0000		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0041
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0114
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0030
Prostate	Prostate	0.0137
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 28

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0026	0.0000 undef
Breast	0.0090	0.0038	2.3818 0.4198
Small intestine	0.0031	0.0000	undef 0.0000
Ovary	0.0000	0.0156	0.0000 undef
Endocrine tissue	0.0119	0.0100	1.1887 0.8413
Gastrointestinal	0.0038	0.0000	undef 0.0000
Brain	0.0015	0.0031	0.4800 2.0835
Hematopoietic	0.0027	0.0000	undef 0.0000
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0011	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0010	0.0041	0.2540 3.9367
Stomach-esophagus	0.0034	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0017	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0109	0.0043	2.5591 0.3908
Prostate	0.0068	0.0528	0.1280 7.8106
Uterus-endometrium	0.0000	0.0136	0.0000 undef
Uterus-myometrium	0.0000	0.0000	undef undef
Uterus-general	0.0059		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0213		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0136
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0101
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0076
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0032
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0030
Prostate	Prostate 0.0137
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 29

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0020	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0021	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0009			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0023
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0032
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0020
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 30

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0078	0.0026	3.0509 0.3278
Breast	0.0038	0.0113	0.3403 2.9389
Small intestine	0.0123	0.0000	undef 0.0000
Ovary	0.0030	0.0702	0.0426 23.4526
Endocrine tissue	0.0017	0.0000	undef 0.0000
Gastrointestinal	0.0556	0.0278	2.0018 0.4995
Brain	0.0000	0.0010	0.0000 undef
Hematopoietic	0.0013	0.0000	undef 0.0000
Skin	0.0000	0.0323	0.0000 undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0062	0.0082	0.7621 1.3122
Lung	0.0097	0.0077	1.2605 0.7933
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0110	0.0000 undef
Pancreas	0.0065	0.0255	0.2559 3.9077
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0192		
Uterus-general	0.0357		
Breast hyperplasia	0.0890		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0213		
White blood cells			
Cervix			

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.0167
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0077
Testicles	0.0082
Lung	0.0000
Nerves	0.0137
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 31

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0026	1.5254 0.6555
Breast	0.0000	0.0019	0.0000 undef
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0130	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0000	0.0010	0.0000 undef
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0037	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0032	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0021	0.0123	0.1693 5.9051
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0000		
Uterus-general	0.0000		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs			
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	
Uterus_n	

Electronic Northern for SEQ. ID NO.: 32

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0038	0.0075	0.5104 1.9593
Small intestine	0.0031	0.0000	undef 0.0000
Ovary	0.0000	0.0156	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0077	0.0000	undef 0.0000
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0010	0.0000	undef 0.0000
Lung	0.0000	0.0153	0.0000 undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0022	0.0000	undef 0.0000
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0000		
Uterus-general	0.0000		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0118		
Seminal vesicle	0.0000		
Sensory organs	0.0000		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0042
Uterus_n	

Electronic Northern for SEQ. ID NO.: 33

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0663	0.0741	0.8942	1.1183
Breast	0.0640	0.0846	0.7561	1.3225
Small intestine	0.1104	0.0165	6.6733	0.1499
Ovary	0.0958	0.1951	0.4912	2.0358
Endocrine tissue	0.0511	0.0426	1.1987	0.8343
Gastrointestinal	0.1188	0.1527	0.7781	1.2851
Brain	0.0584	0.0863	0.6771	1.4769
Hematopoietic	0.1016	0.1136	0.8940	1.1186
Skin	0.0698	0.0000	undef	0.0000
Hepatic	0.0048	0.0776	0.0613	16.3199
Heart	0.1304	0.0000	undef	0.0000
Testicles	0.0230	0.0819	0.2811	3.5571
Lung	0.1620	0.1227	1.3209	0.7571
Stomach-esophagus	0.0580	0.1073	0.5402	1.8511
Muscle-skeleton	0.1045	0.0480	2.1773	0.4593
Kidney	0.0516	0.0959	0.5381	1.8583
Pancreas	0.0529	0.1491	0.3545	2.8205
Penis	0.0749	0.0800	0.9360	1.0684
Prostate	0.0632	0.0426	1.4843	0.6737
Uterus-endometrium	0.0676	0.0000	undef	0.0000
Uterus-myometrium	0.1067	0.2309	0.4621	2.1640
Uterus-general	0.1528	0.0000	undef	0.0000
Breast hyperplasia	0.0480			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0534			
Sensory organs	0.0235			
White blood cells	0.1309			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.1595
Hematopoietic	Endocrine tissue	0.0152
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0052
Heart-blood vessels	Hematopoietic	0.0244
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0097
Kidney	Lung	0.0000
Placenta	Nerves	0.0573
Prostate	Prostate	0.0181
Sensory organs	Sensory Organs	0.0342
	Uterus_n	0.0000
		0.0333

Electronic Northern for SEQ. ID NO.: 34

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0598	0.0501	19.9782
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0030	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0042	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0299	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0106			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 35

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0038	0.0000	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0015	0.0062	0.2400	4.1669
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0052	0.0061	0.8467	1.1810
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0060	0.0000	undef
Muscle-skeleton	0.027	0.0000	undef	0.0000
Kidney	0.0000	0.0110	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 36

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0000	undef	0.0000
Small intestine	0.0026	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0139	0.0000	undef
Hematopoietic	0.0022	0.0000	undef	0.0000
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0137	0.0000	undef
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency
Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0254
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0000
Nerves	0.0020
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 38

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0234	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.3189	0.0153	20.7988	0.0481
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0083
	Uterus_n

Electronic Northern for SEQ. ID NO.: 39

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0286	0.0000	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0030	0.0072	0.4114	2.4307
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0097	0.0077	1.2605	0.7933
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0054	0.0137	0.3965	2.5219
Kidney	0.0033	0.0000	undef	0.0000
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0068	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	0.0000
Uterus-general	0.0059			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0043			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency
Development	
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0036
Kidney	0.0000
Placenta	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0114
Skin-muscle	0.0097
Testicles	0.0000
Lung	0.0082
Nerves	0.0020
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0291

Electronic Northern for SEQ. ID NO.: 40

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0051	0.0056	0.9074	1.1021
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0208	0.1439	6.9489
Gastrointestinal	0.0102	0.0025	4.0755	0.2454
Brain	0.0115	0.0093	1.2425	0.8048
Hematopoietic	0.0044	0.0062	0.7200	1.3890
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0061	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0120	0.1428	7.0040
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	
Gastrointestinal	0.0139
Brain	0.0111
Hematopoietic	0.0063
Skin	0.0039
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0247
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0000
Testicles	0.0164
Lung	0.0070
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0167
Uterus_n	

Electronic Northern for SEQ. ID NO.: 41

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 42

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0034	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0068	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0064	0.0000	undef	undef
Uterus-general	0.0059			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0023
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0114
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0164
Placenta	Nerves	0.0010
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 43

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 44

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0260	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 45

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0000	0.0102	0.0000 undef
Breast	0.0090	0.0056	1.5879 0.6298
Small intestine	0.0031	0.0000	undef 0.0000
Ovary	0.0060	0.0390	0.1535 6.5146
Endocrine tissue	0.0034	0.0025	1.3585 0.7361
Gastrointestinal	0.0019	0.0231	0.0828 12.0723
Brain	0.0000	0.0031	0.0000 undef
Hematopoietic	0.0080	0.0000	undef 0.0000
Skin	0.0037	0.0847	0.0433 23.0839
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0117	0.0000 undef
Lung	0.0021	0.0102	0.2032 4.9209
Stomach-esophagus	0.0017	0.0077	0.0000 undef
Muscle-skeleton	0.0054	0.0000	undef 0.0000
Kidney	0.0000	0.0110	0.0000 undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0065	0.0000	undef 0.0000
Prostate	0.0135	0.0000	undef 0.0000
Uterus-endometrium	0.0229	0.0068	3.3668 0.2970
Uterus-myometrium	0.0000	0.0000	undef undef
Uterus-general	0.0059		
Breast hyperplasia	0.0089		
Prostate hyperplasia	0.0118		
Seminal vesicle	0.0000		
Sensory organs	0.0000		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0012
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0491
Placenta	Nerves	0.0010
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 46

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0117	0.0102	1.1441 0.8741
Breast	0.0090	0.0263	0.3403 2.9389
Small intestine	0.0184	0.0000	undef 0.0000
Ovary	0.0000	0.0156	0.0000 undef
Endocrine tissue	0.0170	0.0050	3.3962 0.2944
Gastrointestinal	0.0172	0.0046	3.7275 0.2683
Brain	0.0081	0.0216	0.3771 2.6517
Hematopoietic	0.0027	0.0000	undef 0.0000
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0048	0.0065	0.7353 1.3600
Heart	0.0117	0.0000	undef 0.0000
Testicles	0.0083	0.0020	undef undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0120	0.0060	1.9989 0.5003
Muscle-skeleton	0.0081	0.0068	1.1896 0.8406
Kidney	0.0017	0.0110	0.1496 6.6857
Pancreas	0.0060	0.0000	undef 0.0000
Penis	0.0131	0.0021	6.1418 0.1628
Prostate	0.0135	0.0000	undef 0.0000
Uterus-endometrium	0.0229	0.0000	undef 0.0000
Uterus-myometrium	0.0102	0.0000	undef 0.0000
Uterus-general	0.0064		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0043		
Sensory organs	0.0106		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0012
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0171
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0137
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n

Electronic Northern for SEQ. ID NO.: 47

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0117	0.0051	2.2882 0.4370
Breast	0.0090	0.0019	4.7637 0.2099
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0030	0.0208	0.1439 6.9489
Endocrine tissue	0.0034	0.0025	1.3585 0.7361
Gastrointestinal	0.0057	0.0000	undef 0.0000
Brain	0.0007	0.0021	0.3600 2.7779
Hematopoietic	0.0013	0.0000	undef 0.0000
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0053	0.0000	undef 0.0000
Testicles	0.0058	0.0000	undef 0.0000
Lung	0.0052	0.0041	1.2701 0.7873
Stomach-esophagus	0.0017	0.0180	0.0952 10.5060
Muscle-skeleton	0.0054	0.0000	undef 0.0000
Kidney	0.0083	0.0055	1.4957 0.6686
Pancreas	0.0090	0.0000	undef 0.0000
Penis	0.0000	0.0064	0.0000 undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0064		
Uterus-general	0.0059		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0118		
Seminal vesicle	0.0017		
Sensory organs	0.0106		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0020
Nerves	0.0000
Prostate	0.0077
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 48

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0026	6.1018	0.1639
Breast	0.0179	0.0169	1.0586	0.9446
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0286	0.2093	4.7774
Endocrine tissue	0.0324	0.0251	1.2906	0.7749
Gastrointestinal	0.0287	0.0278	1.0354	0.9658
Brain	0.0229	0.0164	1.3949	0.7169
Hematopoietic	0.0107	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0350	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0239	0.0225	1.0623	0.9414
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0190	0.0137	1.3878	0.7206
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0262	0.0085	3.0709	0.3256
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0051	0.0000	3.3668	0.2970
Uterus-general	0.0160		undef	0.0000
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0356			
Seminal vesicle	0.0000			
Sensory organs	0.0208			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.1595
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0082
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0162
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0164
Placenta	Nerves	0.0221
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0155
	Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 49

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0051	0.7627 1.3111
Breast	0.0038	0.0056	0.6805 1.4694
Small intestine	0.0031	0.0165	0.1854 5.3946
Ovary	0.0000	0.0130	0.0000 undef
Endocrine tissue	0.0051	0.0025	2.0377 0.4907
Gastrointestinal	0.0057	0.0139	0.4142 2.4145
Brain	0.0037	0.0062	0.6000 1.6668
Hematopoietic	0.0053	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0042	0.0275	0.1542 6.4853
Heart	0.0115	0.0000	undef 0.0000
Testicles	0.0021	0.0041	0.5080 1.9684
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0017	0.0000	undef 0.0000
Muscle-skeleton	0.0109	0.0137	0.7930 1.2610
Kidney	0.0066	0.0055	1.1966 0.8357
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0044	0.0064	0.6824 1.4654
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0051	0.0068	0.0000 undef
Uterus-myometrium	0.0064	0.0000	undef 0.0000
Uterus-general	0.0208		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0017		
Seminal vesicle	0.0000		
Sensory organs			
White blood cells			
Cervix			

	FETUS % frequency
Development	
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0039
Hepatic	0.0000
Heart-blood vessels	0.0260
Lung	0.0000
Suprarenal gland	0.0036
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0020
Nerves	0.0205
Prostate	0.0000
Sensory Organs	0.0042
Uterus_n	

Electronic Northern for SEQ. ID NO.: 50

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0078	0.0179	0.4358 2.2944
Breast	0.0064	0.0094	0.6805 1.4694
Small intestine	0.0092	0.0000	undef 0.0000
Ovary	0.0000	0.0130	0.0000 undef
Endocrine tissue	0.0051	0.0075	0.6792 1.4722
Gastrointestinal	0.0057	0.0000	undef 0.0000
Brain	0.0052	0.0051	1.0079 0.9921
Hematopoietic	0.0080	0.0379	0.2117 4.7230
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0048	0.0000	undef 0.0000
Heart	0.0064	0.0000	undef 0.0000
Testicles	0.0173	0.0117	1.4759 0.6775
Lung	0.0073	0.0102	0.7112 1.4060
Stomach-esophagus	0.0069	0.0000	undef 0.0000
Muscle-skeleton	0.0027	0.0137	0.1983 5.0439
Kidney	0.0000	0.0055	0.0000 undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0131	0.0064	2.0473 0.4885
Prostate	0.0068	0.0000	undef 0.0000
Uterus-endometrium	0.0000	0.0272	0.0000 undef
Uterus-myometrium	0.0128	0.0000	undef undef
Uterus-general	0.0030		
Breast hyperplasia	0.0089		
Prostate hyperplasia	0.0235		
Seminal vesicle	0.0043		
Sensory organs	0.0213		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	
Gastrointestinal	0.0000
Brain	0.0056
Hematopoietic	0.0188
Skin	0.0079
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0087
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0194
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0100
Nerves	0.0000
Prostate	0.0077
Sensory Organs	0.0167
Uterus_n	

Electronic Northern for SEQ. ID NO.: 51

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0000	0.0077	0.0000 undef
Breast	0.0026	0.0150	0.1701 5.8778
Small intestine	0.0061	0.0165	0.3707 2.6973
Ovary	0.0030	0.0208	0.1439 6.9489
Endocrine tissue	0.0119	0.0075	1.5849 0.6309
Gastrointestinal	0.0000	0.0000	undef undef
Brain	0.0037	0.0072	0.5143 1.9446
Hematopoietic	0.0013	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0074	0.0000	0.0000 undef
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0062	0.0061	1.0161 0.9842
Lung	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0188	0.0060	3.1411 0.3184
Muscle-skeleton	0.0027	0.0000	undef 0.0000
Kidney	0.0000	0.0055	0.0000 undef
Pancreas	0.0090	0.0267	0.3369 2.9678
Penis	0.0153	0.0106	1.4331 0.6978
Prostate	0.0135	0.0000	undef 0.0000
Uterus-endometrium	0.0076	0.0068	1.1223 0.8911
Uterus-myometrium	0.0153	0.0000	undef 0.0000
Uterus-general	0.0032		
Breast hyperplasia	0.0178		
Prostate hyperplasia	0.0089		
Seminal vesicle	0.0000		
Sensory organs	0.0026		
White blood cells	0.0106		
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0136
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0052
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0456
Lung	Skin-muscle 0.0065
Suprarenal gland	Testicles 0.0077
Kidney	Lung 0.0164
Placenta	Nerves 0.0040
Prostate	Prostate 0.0068
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 52

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0102	0.3814 2.6222
Breast	0.0179	0.0038	4.7637 0.2099
Small intestine	0.0092	0.0496	0.1854 5.3946
Ovary	0.0060	0.0260	0.2303 4.3431
Endocrine tissue	0.0153	0.0251	0.6113 1.6358
Gastrointestinal	0.0211	0.0463	0.4556 2.1950
Brain	0.0155	0.0103	1.5119 0.6614
Hematopoietic	0.0040	0.0758	0.0529 18.8919
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0388	0.0000 undef
Heart	0.0106	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0177	0.0143	1.2338 0.8105
Stomach-esophagus	0.0069	0.0000	0.0000 undef
Muscle-skeleton	0.0109	0.0274	0.3965 2.5219
Kidney	0.0231	0.0221	1.0470 0.9551
Pancreas	0.0090	0.0267	0.3369 2.9678
Penis	0.0065	0.0106	0.6142 1.6282
Prostate	0.0135	0.0000	undef 0.0000
Uterus-endometrium	0.0076	0.0204	0.3741 2.6732
Uterus-myometrium	0.0000	0.0000	undef undef
Uterus-general	0.0256		
Breast hyperplasia	0.0089		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0095		
Sensory organs	0.0106		
White blood cells			
Cervix			

FETUS % frequency	
Development	0.0278
Gastrointestinal	0.0056
Brain	0.0125
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0164
Lung	0.0060
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 53

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0234	0.0153	1.5254 0.6555
Breast	0.0115	0.0113	1.0208 0.9796
Small intestine	0.0092	0.0165	0.5561 1.7982
Ovary	0.0090	0.0286	0.3140 3.1849
Endocrine tissue	0.0102	0.0125	0.8151 1.2268
Gastrointestinal	0.0230	0.0278	0.8283 1.2072
Brain	0.0148	0.0144	1.0285 0.9723
Hematopoietic	0.0040	0.0000	undef 0.0000
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0106	0.0275	0.3855 2.5941
Testicles	0.0058	0.0000	undef 0.0000
Lung	0.0125	0.0123	1.0161 0.9842
Stomach-esophagus	0.0000	0.0077	0.0000 undef
Muscle-skeleton	0.0137	0.0120	1.1422 0.8755
Kidney	0.0136	0.0274	0.4956 2.0176
Pancreas	0.0099	0.0110	0.8974 1.1143
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0109	0.0192	0.5687 1.7585
Uterus-endometrium	0.0076	0.0136	0.5611 1.7821
Uterus-myometrium	0.0102	0.0000	undef 0.0000
Uterus-general	0.0032		
Breast hyperplasia	0.0119		
Prostate hyperplasia	0.0089		
Seminal vesicle	0.0118		
Sensory organs	0.0087		
White blood cells	0.0000		
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.1595
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0017
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0020
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 54

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0000	undef 0.0000
Breast	0.0013	0.0038	0.3403 2.9389
Small intestine	0.0031	0.0000	undef 0.0000
Ovary	0.0000	0.0130	0.0000 undef
Endocrine tissue	0.0034	0.0025	1.3585 0.7361
Gastrointestinal	0.0019	0.0000	undef 0.0000
Brain	0.0052	0.0051	1.0079 0.9921
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0032	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0031	0.0020	1.5241 0.6561
Lung	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0017	0.0060	0.2856 3.5020
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0017	0.0221	0.0748 13.3713
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0032		
Uterus-general	0.0000		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0068
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0082
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	0.0260 0.0114
Lung	Hematopoietic 0.0000
Suprarenal gland	Skin-muscle 0.0000
Kidney	Testicles 0.0164
Placenta	Lung 0.0060
Prostate	Nerves 0.0068
Sensory organs	Prostate 0.0000
	Sensory Organs 0.0083
	Uterus_n

Electronic Northern for SEQ. ID NO.: 55

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0204	0.1907 5.2444
Breast	0.0141	0.0150	0.9357 1.0687
Small intestine	0.0061	0.0496	0.1236 8.0920
Ovary	0.0120	0.0364	0.3289 3.0402
Endocrine tissue	0.0085	0.0050	1.6981 0.5889
Gastrointestinal	0.0096	0.0046	2.0708 0.4829
Brain	0.0140	0.0185	0.7600 1.3159
Hematopoietic	0.0067	0.0000	undef 0.0000
Skin	0.0294	0.0000	undef 0.0000
Hepatic	0.0095	0.0065	1.4706 0.6800
Heart	0.0138	0.0412	0.3341 2.9932
Testicles	0.0058	0.0000	undef 0.0000
Lung	0.0156	0.0164	0.9526 1.0498
Stomach-esophagus	0.0193	0.0307	0.6303 1.5866
Muscle-skeleton	0.0103	0.0000	undef 0.0000
Kidney	0.0054	0.0000	undef 0.0000
Pancreas	0.0017	0.0331	0.0499 20.0570
Penis	0.0120	0.0000	undef 0.0000
Prostate	0.0174	0.0234	0.7445 1.3433
Uterus-endometrium	0.0203	0.0000	undef 0.0000
Uterus-myometrium	0.0229	0.0136	1.6834 0.5940
Uterus-general	0.0051	0.0954	0.0534 18.7357
Breast hyperplasia	0.0128		
Prostate hyperplasia	0.0238		
Seminal vesicle	0.0000		
Sensory organs	0.0139		
White blood cells	0.0106		
Cervix			

	FETUS % frequency
Development	0.0139
Gastrointestinal	0.0222
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0036
Lung	0.0072
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0303
Prostate	0.0000
Sensory organs	0.0126

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0304
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0488
Hematopoietic	0.0114
Skin-muscle	0.0162
Testicles	0.0000
Lung	0.0082
Nerves	0.0090
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 56

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0153	0.5085	1.9666
Breast	0.0077	0.0132	0.5833	1.7144
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0072	0.3086	3.2409
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0000	0.0468	0.0000	undef
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0000	0.0276	0.0000	undef
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0065	0.0085	0.7677	1.3026
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0152	0.0068	2.2445	0.4455
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0064			
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0182			
White blood cells	0.0213			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0152
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0012
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0065
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0246
Placenta	Nerves	0.0060
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0042
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 57

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0026	1.5254 0.6555
Breast	0.0128	0.0150	0.8507 1.1756
Small intestine	0.0061	0.0165	0.3707 2.6973
Ovary	0.0030	0.0208	0.1439 6.9489
Endocrine tissue	0.0051	0.0226	0.2264 4.4166
Gastrointestinal	0.0077	0.0000	undef 0.0000
Brain	0.0074	0.0103	0.7200 1.3890
Hematopoietic	0.0174	0.0000	undef 0.0000
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0048	0.0000	undef 0.0000
Heart	0.0085	0.0275	0.3084 3.2426
Testicles	0.0115	0.0000	undef 0.0000
Lung	0.0062	0.0102	0.6096 1.6403
Stomach-esophagus	0.0000	0.0307	0.0000 undef
Muscle-skeleton	0.0120	0.0060	1.9989 0.5003
Kidney	0.0217	0.0068	3.1722 0.3152
Pancreas	0.0017	0.0000	undef 0.0000
Penis	0.0180	0.0000	undef 0.0000
Prostate	0.0044	0.0085	0.5118 1.9538
Uterus-endometrium	0.0068	0.0000	undef 0.0000
Uterus-myometrium	0.0089	0.0000	undef 0.0000
Uterus-general	0.0139	0.0235	0.2806 3.5642
Breast hyperplasia	0.0000	0.0000	undef 0.0000
Prostate hyperplasia	0.0235	0.0139	0.0000 0.0000
Seminal vesicle	0.0000	0.0106	0.0000 undef
Sensory organs	0.0000	0.0000	0.0000 0.0000
White blood cells	0.0000	0.0000	0.0000 0.0000
Cervix	0.0000	0.0000	0.0000 0.0000

FETUS % frequency	
Development	0.0278
Gastrointestinal	0.0056
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0145
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0076
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0077
Testicles	0.0082
Lung	0.0120
Nerves	0.0274
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 58

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0585	0.0332	1.7601	0.5681
Breast	0.0230	0.0132	1.7499	0.5715
Small intestine	0.0153	0.0827	0.1854	5.3946
Ovary	0.0150	0.0546	0.2741	3.6482
Endocrine tissue	0.0136	0.0150	0.9057	1.1042
Gastrointestinal	0.0192	0.0416	0.4602	2.1730
Brain	0.0163	0.0277	0.5866	1.7046
Hematopoietic	0.0374	0.0379	0.9881	1.0121
Skin	0.0404	0.0847	0.4765	2.0985
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0297	0.0412	0.7196	1.3897
Testicles	0.0863	0.1169	0.7380	1.3551
Lung	0.0364	0.0266	1.3678	0.7311
Stomach-esophagus	0.0290	0.0767	0.3782	2.6444
Muscle-skeleton	0.0190	0.0137	1.3878	0.7206
Kidney	0.0132	0.0497	0.2659	3.7607
Pancreas	0.0359	0.0800	0.4493	2.2259
Penis	0.0262	0.0128	2.0473	0.4885
Prostate	0.0338	0.0528	0.6402	1.5621
Uterus-endometrium	0.0229	0.0000	undef	0.0000
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0128			
Breast hyperplasia	0.0178			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0235			
Sensory organs	0.0251			
White blood cells	0.0106			
Cervix				

	FETUS % frequency
Development	0.0278
Gastrointestinal	0.0528
Brain	0.1189
Hematopoietic	0.0275
Skin	0.0000
Hepatic	0.0520
Heart-blood vessels	0.0818
Lung	0.0253
Suprarenal gland	0.0254
Kidney	0.0371
Placenta	0.0424
Prostate	0.0499
Sensory organs	0.0251

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0093
Fetal	0.0366
Gastrointestinal	0.0057
Hematopoietic	0.0389
Skin-muscle	0.0154
Testicles	0.0491
Lung	0.0120
Nerves	0.0068
Prostate	0.0077
Sensory Organs	0.0250
Uterus_n	

Electronic Northern for SEQ. ID NO.: 59

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0060	0.0390	0.1535	6.5146
Endocrine tissue	0.0102	0.0251	0.4075	2.4537
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0140	0.0082	1.7099	0.5848
Hematopoietic	0.0053	0.1515	0.0353	28.3379
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0104	0.0184	0.5645	1.7715
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0051	0.0180	0.2856	3.5020
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0192	0.0000	undef	undef
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0118			
Sensory organs	0.0061			
White blood cells	0.0213			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0203
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0023
Hepatic	Gastrointestinal	0.0244
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0162
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0246
Placenta	Nerves	0.0241
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 63

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0230	0.0000 undef
Breast	0.0000	0.0150	0.0000 undef
Small intestine	0.0675	0.0000	undef 0.0000
Ovary	0.0000	0.0208	0.0000 undef
Endocrine tissue	0.0153	0.0139	1.1045 0.9054
Gastrointestinal	0.0022	0.0154	0.1440 6.9448
Brain	0.0053	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0323	0.0000 undef
Hepatic	0.0064	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0020	0.0000 undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	6.3239	0.7179	8.8087 0.1135
Kidney	0.0030	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0000		
Uterus-general	0.0089		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0106		
Sensory organs			
White blood cells			
Cervix			

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.2721
Brain	0.0063
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0354
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.2685
Hematopoietic	0.0057
Skin-muscle	0.0097
Testicles	0.0000
Lung	0.0082
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 65

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0039	0.0077	0.5085 1.9666
Breast	0.0064	0.0075	0.8507 1.1756
Small intestine	0.0245	0.0165	1.4830 0.6743
Ovary	0.0090	0.0520	0.1727 5.7908
Endocrine tissue	0.0085	0.0000	undef 0.0000
Gastrointestinal	0.0153	0.0324	0.4733 2.1127
Brain	0.0044	0.0123	0.3600 2.7779
Hematopoietic	0.0027	0.0000	undef 0.0000
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0381	0.0970	0.3922 2.5500
Heart	0.0074	0.0137	0.5397 1.8529
Testicles	0.0000	0.0000	undef undef
Lung	0.0052	0.0082	0.6350 1.5747
Stomach-esophagus	0.0000	0.0230	0.0000 undef
Muscle-skeleton	0.0086	0.0000	undef 0.0000
Kidney	0.0163	0.0616	0.2643 3.7829
Pancreas	0.0396	0.0055	7.1795 0.1393
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0065	0.0106	0.6142 1.6282
Uterus-endometrium	0.0000	0.0528	0.0000 undef
Uterus-myometrium	0.0000	0.0068	1.1223 0.8911
Uterus-general	0.0089	0.2863	0.0534 18.7357
Breast hyperplasia	0.0235		
Prostate hyperplasia	0.0043		
Seminal vesicle	0.0319		
Sensory organs			
White blood cells			
Cervix			

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.0222
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Suprarenal gland	0.0254
Kidney	0.0062
Placenta	0.0242
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0245
Fetal	0.0122
Gastrointestinal	0.0228
Hematopoietic	0.0162
Skin-muscle	0.0000
Testicles	0.0082
Lung	0.0010
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0250
Uterus_n	

Electronic Northern for SEQ. ID NO.: 67

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T
			T/N
Bladder	0.0039	0.0102	0.3814 2.6222
Breast	0.0026	0.0169	0.1512 6.6125
Small intestine	0.0092	0.0165	0.5561 1.7982
Ovary	0.0060	0.0260	0.2303 4.3431
Endocrine tissue	0.0034	0.0075	0.4528 2.2083
Gastrointestinal	0.0057	0.0185	0.3106 3.2193
Brain	0.0044	0.0062	0.7200 1.3890
Hematopoietic	0.0094	0.0000	undef 0.0000
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0129	0.0000 undef
Heart	0.0042	0.0000	undef 0.0000
Testicles	0.0115	0.0000	undef 0.0000
Lung	0.0031	0.0102	0.3048 3.2806
Stomach-esophagus	0.0097	0.0153	0.6303 1.5866
Muscle-skeleton	0.0017	0.0060	0.2856 3.5020
Kidney	0.0081	0.0068	1.1896 0.8406
Pancreas	0.0050	0.0055	0.8974 1.1143
Penis	0.0120	0.0000	undef 0.0000
Prostate	0.0022	0.0085	0.2559 3.9077
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0051	0.0000	undef undef
Uterus-general	0.0032	0.0000	undef 0.0000
Breast hyperplasia	0.0059	0.0000	
Prostate hyperplasia	0.0089	0.0235	
Seminal vesicle	0.0061	0.0061	
Sensory organs	0.0106		
White blood cells			
Cervix			

FETUS	% frequency
Development	0.0000
Gastrointestinal	0.0056
Brain	0.0188
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES	% frequency
Breast	0.0272
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0169
Gastrointestinal	0.0000
Hematopoietic	0.0171
Skin-muscle	0.0000
Testicles	0.0328
Lung	0.0080
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0125
Uterus_n	

Electronic Northern for SEQ. ID NO.: 69

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0038	0.0000	0.0000	undef
Gastrointestinal	0.0007	0.0021	0.3600	2.7779
Brain	0.0053	0.0000	undef	0.0000
Hematopoietic	0.0037	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0042	0.0000	undef	0.0000
Heart	0.0288	0.0000	undef	0.0000
Testicles	0.0031	0.0000	undef	0.0000
Lung	0.0097	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0060	0.0000	undef
Muscle-skeleton	0.0054	0.0000	undef	0.0000
Kidney	0.0030	0.0000	undef	0.0000
Pancreas	0.0022	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0102	0.0954	0.1067	9.3678
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0017			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.1595
Brain	Ovary_t	0.0152
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0029
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0342
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0020
Placenta	Nerves	0.0068
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0042
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 70

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0077	0.0094	0.8166	1.2245
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0324	0.0075	4.3019	0.2325
Gastrointestinal	0.0134	0.0093	1.4496	0.6898
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0379	0.1059	9.4460
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0135	0.0102	1.3209	0.7571
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0099	0.0055	1.7949	0.5571
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0096	0.0149		
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0130			
Sensory organs	0.0106			
White blood cells				
Cervix				

	FETUS % frequency
Development	0.0139
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0072
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0097
Testicles	0.0154
Lung	0.0164
Nerves	0.0070
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 72

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.1053	0.0895	1.1768 0.8498
Breast	0.0652	0.0846	0.7713 1.2966
Small intestine	0.1073	0.0992	1.0813 0.9248
Ovary	0.0629	0.1353	0.4649 2.1509
Endocrine tissue	0.0579	0.0451	1.2830 0.7794
Gastrointestinal	0.1379	0.2220	0.6213 1.6096
Brain	0.0702	0.0534	1.3153 0.7603
Hematopoietic	0.1056	0.1136	0.9293 1.0761
Skin	0.0587	0.0847	0.6931 1.4427
Hepatic	0.0285	0.1035	0.2757 3.6266
Heart	0.1293	0.0412	3.1353 0.3189
Testicles	0.0403	0.1754	0.2296 4.3556
Lung	0.0914	0.1063	0.8598 1.1631
Stomach-esophagus	0.0387	0.1840	0.2101 4.7599
Muscle-skeleton	0.0814	0.1438	0.5665 1.7654
Kidney	0.0363	0.1878	0.1936 5.1662
Pancreas	0.1138	0.0800	1.4227 0.7029
Penis	0.0697	0.0958	0.7279 1.3738
Prostate	0.1824	0.0000	undef 0.0000
Uterus-endometrium	0.0838	0.0951	0.8818 1.1341
Uterus-myometrium	0.1171	0.0000	undef 0.0000
Uterus-general	0.0671		
Breast hyperplasia	0.0922		
Prostate hyperplasia	0.0712		
Seminal vesicle	0.0706		
Sensory organs	0.1448		
White blood cells	0.1810		
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0340
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0253
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0163
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0292
Suprarenal gland	Testicles 0.0077
Kidney	Lung 0.0246
Placenta	Nerves 0.0090
Prostate	Prostate 0.0274
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0042

Electronic Northern for SEQ. ID NO.: 73

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0663	0.0895	0.7409 1.3497
Breast	0.0371	0.0489	0.7591 1.3174
Small intestine	0.0766	0.0000	undef 0.0000
Ovary	0.0270	0.0754	0.3573 2.7989
Endocrine tissue	0.0170	0.0326	0.5225 1.9139
Gastrointestinal	0.0805	0.0833	0.9664 1.0348
Brain	0.0177	0.0390	0.4547 2.1992
Hematopoietic	0.0896	0.0758	1.1822 0.8459
Skin	0.0551	0.1695	0.3249 3.0779
Hepatic	0.0238	0.0776	0.3064 3.2640
Heart	0.0604	0.1237	0.4883 2.0480
Testicles	0.0288	0.0702	0.4100 2.4391
Lung	0.0519	0.0429	1.2096 0.8267
Stomach-esophagus	0.0676	0.0843	0.8022 1.2466
Muscle-skeleton	0.0223	0.0240	0.9280 1.0775
Kidney	0.0353	0.0548	0.6443 1.5520
Pancreas	0.0132	0.0773	0.1709 5.8500
Penis	0.0838	0.0533	1.5724 0.6360
Prostate	0.0567	0.0255	2.2179 0.4509
Uterus-endometrium	0.0946	0.0000	undef 0.0000
Uterus-myometrium	0.0762	0.0679	1.1223 0.8911
Uterus-general	0.0407	0.0000	undef 0.0000
Breast hyperplasia	0.0192		
Prostate hyperplasia	0.0505		
Seminal vesicle	0.0445		
Sensory organs	0.0235		
White blood cells	0.0772		
Cervix	0.0106		

	FETUS % frequency
Development	0.0139
Gastrointestinal	0.0305
Brain	0.0313
Hematopoietic	0.0393
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0285
Lung	0.0145
Suprarenal gland	0.0000
Kidney	0.0285
Placenta	0.0679
Prostate	0.0364
Sensory organs	0.0997

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0272
Ovary_n	0.0000
Ovary_t	0.1468
Endocrine tissue	0.0245
Fetal	0.0105
Gastrointestinal	0.0366
Hematopoietic	0.0057
Skin-muscle	0.0292
Testicles	0.0000
Lung	0.0328
Nerves	0.0040
Prostate	0.0068
Sensory Organs	0.0250
Uterus_n	

Electronic Northern for SEQ. ID NO.: 74

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0234	0.0000	undef 0.0000
Breast	0.0000	0.0000	undef undef
Small intestine	0.0000	0.0468	undef undef
Ovary	0.0000	0.0000	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0000	0.0000	undef undef
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0110	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0353	0.0164	2.1591 0.4631
Testicles	0.1836	0.1227	1.4969 0.6681
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0050	0.0221	0.2244 4.4571
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0022	0.0128	0.1706 5.8615
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000		undef undef
Uterus-myometrium	0.0000		
Uterus-general	0.1246		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs			
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 76

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0077	0.0000 undef
Breast	0.0026	0.0301	0.0851 11.7556
Small intestine	0.0000	0.0331	0.0000 undef
Ovary	0.0030	0.0728	0.0411 24.3213
Endocrine tissue	0.0000	0.0100	0.0000 undef
Gastrointestinal	0.0000	0.0046	0.0000 undef
Brain	0.0510	0.0596	0.8565 1.1675
Hematopoietic	0.0040	0.0000	undef 0.0000
Skin	0.0037	0.1695	0.0217 46.1678
Hepatic	0.0523	0.1747	0.2996 3.3382
Heart	0.0138	0.0137	1.0023 0.9977
Testicles	0.0000	0.0935	0.0000 undef
Lung	0.0073	0.0818	0.0889 11.2478
Stomach-esophagus	0.0000	0.0230	0.0000 undef
Muscle-skeleton	0.0240	0.2760	0.0869 11.5066
Kidney	0.3910	0.4108	0.9516 1.0508
Pancreas	0.1123	0.0387	2.9060 0.3441
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0000	0.0021	0.0000 undef
Uterus-endometrium	0.0000	0.2111	0.0320 31.2422
Uterus-myometrium	0.0051	0.0000	undef undef
Uterus-general	0.0064	0.1908	0.0267 37.4714
Breast hyperplasia	0.0059		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0118		
Sensory organs	0.1838		
White blood cells	0.0000		
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0696
Gastrointestinal	0.0194
Brain	0.0000
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0036
Suprarenal gland	0.0254
Kidney	0.0062
Placenta	0.2302
Prostate	0.0000
Sensory organs	0.1632
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0128
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0164
Nerves	0.0231
Prostate	0.0068
Sensory Organs	0.0310
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 78

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T T/N
Bladder	0.0156	0.0153	1.0170 0.9833
Breast	0.0090	0.0244	0.3664 2.7290
Small intestine	0.0123	0.0496	0.2472 4.0460
Ovary	0.0090	0.0338	0.2657 3.7640
Endocrine tissue	0.0136	0.0226	0.6038 1.6562
Gastrointestinal	0.0044	0.0216	0.2057 4.8614
Brain	0.0254	0.0000	undef 0.0000
Hematopoietic	0.0110	0.0000	undef 0.0000
Skin	0.0048	0.0065	0.7353 1.3600
Hepatic	0.0170	0.0137	1.2336 0.8107
Heart	0.0000	0.0000	undef undef
Testicles	0.0073	0.0286	0.2540 3.9367
Lung	0.0000	0.0307	0.0000 undef
Stomach-esophagus	0.0051	0.0180	0.2856 3.5020
Muscle-skeleton	0.0190	0.0068	2.7756 0.3603
Kidney	0.0083	0.0110	0.7479 1.3371
Pancreas	0.0120	0.0267	0.4493 2.2259
Penis	0.0131	0.0106	1.2284 0.8141
Prostate	0.0135	0.0000	undef 0.0000
Uterus-endometrium	0.0076	0.0136	0.5611 1.7821
Uterus-myometrium	0.0051	0.0000	undef 0.0000
Uterus-general	0.0192		
Breast hyperplasia	0.0030		
Prostate hyperplasia	0.0089		
Seminal vesicle	0.0118		
Sensory organs	0.0113		
White blood cells	0.0213		
Cervix			

	FETUS % frequency
Development	0.0139
Gastrointestinal	0.0250
Brain	0.0063
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0178
Lung	0.0145
Suprarenal gland	0.0000
Kidney	0.0371
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0377

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0256
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0309
Lung	0.0164
Nerves	0.0100
Prostate	0.0068
Sensory Organs	0.1084
Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 79

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0273	0.0332	0.8214 1.2174
Breast	0.0230	0.0188	1.2250 0.8164
Small intestine	0.0276	0.0331	0.8342 1.1988
Ovary	0.0210	0.0650	0.3224 3.1022
Endocrine tissue	0.0238	0.0276	0.8645 1.1567
Gastrointestinal	0.0172	0.0463	0.3728 2.6827
Brain	0.0118	0.0144	0.8228 1.2153
Hematopoietic	0.0214	0.0379	0.5646 1.7711
Skin	0.0147	0.0000	undef 0.0000
Hepatic	0.0048	0.0259	0.1838 5.4400
Heart	0.0540	0.0550	0.9830 1.0173
Testicles	0.0173	0.0585	0.2952 3.3877
Lung	0.0322	0.0450	0.7159 1.3969
Stomach-esophagus	0.0290	0.0077	3.7816 0.2644
Muscle-skeleton	0.0240	0.0600	0.3998 2.5014
Kidney	0.0353	0.0548	0.6443 1.5520
Pancreas	0.0165	0.0221	0.7479 1.3371
Penis	0.0150	0.0267	0.5616 1.7807
Prostate	0.0240	0.0405	0.5926 1.6874
Uterus-endometrium	0.0270	0.1055	0.2561 3.9053
Uterus-myometrium	0.0381	0.0068	5.6113 0.1782
Uterus-general	0.0051	0.1908	0.0267 37.4714
Breast hyperplasia	0.0224		
Prostate hyperplasia	0.0297		
Seminal vesicle	0.0534		
Sensory organs	0.0588		
White blood cells	0.0234		
Cervix	0.0106		

	FETUS % frequency
Development	0.0557
Gastrointestinal	0.0083
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0253
Suprarenal gland	0.0507
Kidney	0.0432
Placenta	0.0303
Prostate	0.1247
Sensory organs	0.0251

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0245
Fetal	0.0256
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0583
Testicles	0.0231
Lung	0.0491
Nerves	0.0221
Prostate	0.0821
Sensory Organs	0.0000
Uterus_n	0.0416

Electronic Northern for SEQ. ID NO.: 80

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0000	undef 0.0000
Breast	0.0026	0.0075	0.3403 2.9389
Small intestine	0.0061	0.0000	undef 0.0000
Ovary	0.0030	0.0182	0.1645 6.0803
Endocrine tissue	0.0017	0.0025	0.6792 1.4722
Gastrointestinal	0.0000	0.0139	0.0000 undef
Brain	0.0044	0.0041	1.0799 0.9260
Hematopoietic	0.0027	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef 0.0000
Heart	0.0021	0.0000	0.4920 2.0326
Testicles	0.0058	0.0117	0.5080 1.9684
Lung	0.0010	0.0020	undef undef
Stomach-esophagus	0.0000	0.0000	0.0000 undef
Muscle-skeleton	0.0054	0.0000	undef 0.0000
Kidney	0.0033	0.0055	0.5983 1.6714
Pancreas	0.0000	0.0000	undef undef
Penis	0.0044	0.0000	undef 0.0000
Prostate	0.0000	0.0068	0.0000 undef
Uterus-endometrium	0.0102	0.0000	undef 0.0000
Uterus-myometrium	0.0064		
Uterus-general	0.0059		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0017		
Sensory organs	0.0106		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0254
Suprarenal gland	0.0062
Kidney	0.0000
Placenta	0.0000
Prostate	0.0126
Sensory organs	
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0093
Gastrointestinal	0.0114
Hematopoietic	0.0000
Skin-muscle	0.0309
Testicles	0.0082
Lung	0.0060
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 81

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0141	0.0150	0.9357	1.0687
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0090	0.0416	0.2159	4.6326
Endocrine tissue	0.0119	0.0176	0.6792	1.4722
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0126	0.0031	4.0798	0.2451
Hematopoietic	0.0080	0.1136	0.0706	14.1689
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0191	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0104	0.0164	0.6350	1.5747
Stomach-esophagus	0.0069	0.0120	0.5711	1.7510
Muscle-skeleton	0.0109	0.0137	0.7930	1.2610
Kidney	0.0033	0.0000	undef	0.0000
Pancreas	0.0090	0.0267	0.3369	2.9678
Penis	0.0131	0.0021	6.1418	0.1628
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0136	0.0000	0.0000
Uterus-myometrium	0.0128	0.0000	undef	undef
Uterus-general	0.0119			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0104			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0278
Gastrointestinal	0.0111
Brain	0.0250
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0285
Heart-blood vessels	0.0108
Lung	0.0254
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0377
Sensory organs	
Breast	0.0000
Ovary_n	0.1595
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0057
Hematopoietic	0.0065
Skin-muscle	0.0231
Testicles	0.0082
Lung	0.0191
Nerves	0.0068
Prostate	0.0155
Sensory Organs	0.0250
Uterus_n	

Electronic Northern for SEQ. ID NO.: 82

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0351	0.0435	0.8076	1.2383
Breast	0.0576	0.0489	1.1778	0.8490
Small intestine	0.0337	0.0165	2.0391	0.4904
Ovary	0.0659	0.1353	0.4871	2.0531
Endocrine tissue	0.0801	0.0878	0.9121	1.0963
Gastrointestinal	0.0441	0.1203	0.3664	2.7294
Brain	0.1072	0.0298	3.5998	0.2778
Hematopoietic	0.0201	0.1515	0.1323	7.5568
Skin	0.0661	0.0000	undef	0.0000
Hepatic	0.0428	0.0582	0.7353	1.3600
Heart	0.0572	0.0687	0.8327	1.2010
Testicles	0.0460	0.1988	0.2315	4.3193
Lung	0.0416	0.0634	0.6555	1.5255
Stomach-esophagus	0.0290	0.0613	0.4727	2.1155
Muscle-skeleton	0.0360	0.0180	1.9989	0.5003
Kidney	0.0489	0.0411	1.1896	0.8406
Pancreas	0.1371	0.0552	2.4829	0.4028
Penis	0.0479	0.0000	undef	0.0000
Prostate	0.0741	0.0426	1.7402	0.5747
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0534	0.0475	1.1223	0.8911
Uterus-general	0.0407	0.0000	undef	0.0000
Breast hyperplasia	0.0639			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0623			
Sensory organs	0.0588			
White blood cells	0.0546			
Cervix	0.0106			

	FETUS % frequency
Development	0.0696
Gastrointestinal	0.1971
Brain	0.0500
Hematopoietic	0.0551
Skin	0.0000
Hepatic	0.1040
Heart-blood vessels	0.0427
Lung	0.1120
Suprarenal gland	0.0427
Kidney	0.1521
Placenta	0.0309
Prostate	0.1212
Sensory organs	0.0748
	0.0628

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0304
Endocrine tissue	0.0000
Fetal	0.0262
Gastrointestinal	0.1220
Hematopoietic	0.0285
Skin-muscle	0.0356
Testicles	0.0309
Lung	0.2211
Nerves	0.0502
Prostate	0.0615
Sensory Organs	0.1471
Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 83

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0077	2.0339	0.4917
Breast	0.0307	0.0169	1.8147	0.5510
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0120	0.0416	0.2878	3.4745
Endocrine tissue	0.0273	0.0176	1.5526	0.6441
Gastrointestinal	0.0153	0.0324	0.4733	2.1127
Brain	0.0192	0.0154	1.2479	0.8013
Hematopoietic	0.0147	0.0379	0.3882	2.5762
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0238	0.0065	3.6765	0.2720
Heart	0.0170	0.0137	1.2336	0.8107
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0177	0.0204	0.8637	1.1579
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0154	0.0060	2.5700	0.3891
Kidney	0.0190	0.0000	undef	0.0000
Pancreas	0.0132	0.0166	0.7977	1.2536
Penis	0.0240	0.0000	undef	0.0000
Prostate	0.0109	0.0106	1.0236	0.9769
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0000	undef	0.0000
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0416			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0178			
Sensory organs	0.0235			
White blood cells	0.0087			
Cervix	0.0213			

FETUS % frequency	
Development	
Gastrointestinal	0.0278
Brain	0.0056
Hematopoietic	0.0438
Skin	0.0039
Hepatic	0.0000
Heart-blood vessels	0.0427
Lung	0.0145
Suprarenal gland	0.0254
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0377

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0068
Ovary_n	0.1595
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0111
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles	0.0000
Lung	0.0491
Nerves	0.0231
Prostate	0.0342
Sensory Organs	0.0000
Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 84

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0312	0.0153	2.0339	0.4917
Breast	0.0192	0.0320	0.6005	1.6654
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0060	0.0416	0.1439	6.9489
Endocrine tissue	0.0273	0.0451	0.6038	1.6562
Gastrointestinal	0.0230	0.0093	2.4850	0.4024
Brain	0.0177	0.0164	1.0799	0.9260
Hematopoietic	0.0174	0.0379	0.4587	2.1798
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0381	0.0065	5.8824	0.1700
Heart	0.0159	0.0000	undef	0.0000
Testicles	0.0115	0.0351	0.3280	3.0489
Lung	0.0187	0.0123	1.5241	0.6561
Stomach-esophagus	0.0120	0.0460	0.0000	undef
Muscle-skeleton	0.0109	0.0205	0.5287	1.8915
Kidney	0.0083	0.0166	0.4986	2.0057
Pancreas	0.0180	0.0000	undef	0.0000
Penis	0.0131	0.0064	2.0473	0.4885
Prostate	0.0405	0.0528	0.7682	1.3018
Uterus-endometrium	0.0305	0.0204	1.4964	0.6683
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0128			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0165			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0272
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0152
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0151
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0259
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0246
Kidney	Lung	0.0341
Placenta	Nerves	0.0274
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0125
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 85

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0102	0.0000	undef
Breast	0.0051	0.0395	0.1296	7.7146
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0030	0.0312	0.0959	10.4234
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0038	0.0139	0.2761	3.6217
Brain	0.0081	0.0113	0.7200	1.3890
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0062	0.0020	3.0482	0.3281
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0034	0.0120	0.2856	3.5020
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0030	0.1066	0.0281	35.6140
Prostate	0.0044	0.0043	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0026			
Sensory organs	0.0106			
White blood cells				
Cervix				

	FETUS % frequency
Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0039
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0087
Gastrointestinal	0.0244
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0082
Nerves	0.0010
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0333

Electronic Northern for SEQ. ID NO.: 88

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0486	0.4014	2.4911
Breast	0.0064	0.0338	0.1890	5.2900
Small intestine	0.0153	0.0165	0.9268	1.0789
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0136	0.0000	undef	0.0000
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0052	0.0123	0.4200	2.3811
Hematopoietic	0.0361	0.0379	0.9528	1.0496
Skin	0.0184	0.0847	0.2166	4.6168
Hepatic	0.0048	0.0388	0.1225	8.1599
Heart	0.0074	0.0962	0.0771	12.9706
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0665	0.0573	1.1612	0.8612
Stomach-esophagus	0.0193	0.0383	0.5042	1.9833
Muscle-skeleton	0.0788	0.0300	2.6271	0.3807
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0116	0.0166	0.6980	1.4326
Penis	0.0000	0.0800	0.0000	undef
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0954	0.0000	undef
Uterus-general	0.0128			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.1682			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0557
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0064
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0032
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0125
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 89

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0153	0.0038	4.0832	0.2449
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0068	0.0025	2.7170	0.3681
Gastrointestinal	0.0077	0.0046	1.6567	0.6036
Brain	0.0052	0.0021	2.5199	0.3968
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0844	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0201	0.0275	0.7324	1.3653
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0156	0.0061	2.5402	0.3937
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0050	0.0000	undef	0.0000
Pancreas	0.0329	0.1066	0.8974	1.1143
Penis	0.0022	0.0021	0.3089	3.2376
Prostate	0.0000	0.0000	1.0236	0.9769
Uterus-endometrium	0.0076	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	0.0000
Uterus-general	0.0032	0.0000	undef	0.0000
Breast hyperplasia	0.0089	0.0118	0.0852	
Prostate hyperplasia	0.0121			
Seminal vesicle				
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency
Development	
Gastrointestinal	0.0139
Brain	0.0028
Hematopoietic	0.0063
Skin	0.0079
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0107
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0087
Fetal	0.0244
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0154
Testicles	0.0164
Lung	0.0020
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0125
Uterus_n	

Electronic Northern for SEQ. ID NO.: 90

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0169	0.2268	4.4083
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0051	0.0326	0.1567	6.3796
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0067	0.0062	1.0799	0.9260
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0083	0.0143	0.5806	1.7223
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0109	0.0137	0.7930	1.2610
Kidney	0.0033	0.0000	undef	0.0000
Pancreas	0.0120	0.0000	undef	0.0000
Penis	0.0065	0.0128	0.5118	1.9538
Prostate	0.0076	0.0068	undef	undef
Uterus-endometrium	0.0102	0.0000	1.1223	0.8911
Uterus-myometrium	0.0000		undef	0.0000
Uterus-general	0.0059			
Breast hyperplasia	0.0356			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0052			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0064
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0057
Heart-blood vessels	Hematopoietic 0.0130
Lung	Skin-muscle 0.0231
Suprarenal gland	Testicles 0.0164
Kidney	Lung 0.0060
Placenta	Nerves 0.0137
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0042
	Uterus_n

Electronic Northern for SEQ. ID NO.: 91

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0119	0.0150	0.7925	1.2619
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0081	0.0082	0.9899	1.0102
Hematopoietic	0.0120	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0127	0.0412	0.3084	3.2426
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0073	0.0307	0.2371	4.2179
Stomach-esophagus	0.0290	0.0383	0.7563	1.3222
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0054	0.0274	0.1983	5.0439
Pancreas	0.0033	0.0166	0.1994	5.0142
Penis	0.0150	0.0533	0.2808	3.5614
Prostate	0.0000	0.0106	0.0000	undef
Uterus-endometrium	0.0076	0.0068	undef	undef
Uterus-myometrium	0.0051	0.0000	1.1223	0.8911
Uterus-general	0.0064		undef	0.0000
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0106			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0130
Testicles	0.0000
Lung	0.0328
Nerves	0.0040
Prostate	0.0274
Sensory Organs	0.0000
Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 92

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0132	0.2917	3.4287
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0000	0.0000	undef	undef
Lung	0.0145	0.0061	2.3708	0.4218
Stomach-esophagus	0.0017	0.0153	0.0000	undef
Muscle-skeleton	0.0054	0.0000	undef	0.0000
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0000	undef	undef
Uterus-myometrium	0.0032	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0139			
Sensory organs	0.0106			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0047
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0065
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0164
Placenta	Nerves	0.0040
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 93

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0153	0.0000	undef
Breast	0.0077	0.0113	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0286	0.1047	9.5548
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0059	0.0082	0.7200	1.3890
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0021	0.0061	0.3387	2.9526
Stomach-esophagus	0.0051	0.0000	undef	undef
Muscle-skeleton	0.0054	0.0068	0.7930	1.2610
Kidney	0.0017	0.0331	0.0499	20.0570
Pancreas	0.0090	0.0267	0.3369	2.9678
Penis	0.0044	0.0021	2.0473	0.4885
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0032	0.0000		
Breast hyperplasia	0.0000	0.0000		
Prostate hyperplasia	0.0000	0.0000		
Seminal vesicle	0.0009	0.0000		
Sensory organs	0.0000	0.0000		
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0116
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0114
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0082
Kidney	Lung	0.0070
Placenta	Nerves	0.0068
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0125
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 94

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0051	0.0000 undef
Breast	0.0115	0.0132	0.8750 1.1429
Small intestine	0.0337	0.0496	0.6797 1.4713
Ovary	0.0030	0.0390	0.0768 13.0292
Endocrine tissue	0.0085	0.0251	0.3396 2.9444
Gastrointestinal	0.0747	0.0879	0.8501 1.1763
Brain	0.0007	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0048	0.0194	0.2451 4.0800
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0351	0.0000 undef
Testicles	0.0042	0.0143	0.2903 3.4446
Lung	0.0483	0.0077	6.3027 0.1587
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0163	0.0137	1.1896 0.8406
Kidney	0.0231	0.0166	1.3960 0.7163
Pancreas	0.0000	0.0000	undef undef
Penis	0.0065	0.0106	0.6142 1.6282
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0064		
Uterus-general	0.0119		
Breast hyperplasia	0.0089		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0106		
White blood cells			
Cervix			

FETUS % frequency	
Development	
Gastrointestinal	0.0000
Brain	0.0083
Hematopoietic	0.0188
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0108
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Breast	
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0246
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 95

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1092	0.0460	2.3729	0.4214
Breast	0.0627	0.0865	0.7249	1.3795
Small intestine	0.1012	0.1158	0.8739	1.1443
Ovary	0.0599	0.1509	0.3970	2.5190
Endocrine tissue	0.0852	0.2984	0.2854	3.5039
Gastrointestinal	0.0900	0.0925	0.9733	1.0274
Brain	0.1811	0.0637	2.8450	0.3515
Hematopoietic	0.0521	0.1136	0.4587	2.1798
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0809	0.0582	1.3889	0.7200
Heart	0.1092	0.0962	1.1344	0.8815
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0634	0.1104	0.5739	1.7425
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0463	0.0420	1.1014	0.9079
Kidney	0.0706	0.1369	0.5155	1.9400
Pancreas	0.0743	0.1049	0.7085	1.4114
Penis	0.1467	0.0800	1.8345	0.5451
Prostate	0.0567	0.0873	0.6491	1.5405
Uterus-endometrium	0.0811	0.0000	undef	0.0000
Uterus-myometrium	0.1067	0.1155	0.9242	1.0820
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.1407			
Prostate hyperplasia	0.0713			
Seminal vesicle	0.0534			
Sensory organs	0.0353			
White blood cells	0.0390			
Cervix	0.0532			

FETUS % frequency	
Development	
Gastrointestinal	0.1113
Brain	0.0694
Hematopoietic	0.0938
Skin	0.0590
Hepatic	0.0000
Heart-blood vessels	0.0260
Lung	0.1281
Suprarenal gland	0.0397
Kidney	0.0507
Placenta	0.0432
Prostate	0.0485
Sensory organs	0.0499
	0.1381

STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Breast	
Ovary_n	0.0068
Ovary_t	0.0000
Endocrine tissue	0.0253
Fetal	0.0000
Gastrointestinal	0.0116
Hematopoietic	0.0122
Skin-muscle	0.0000
Testicles	0.0454
Lung	0.0077
Nerves	0.0246
Prostate	0.0753
Sensory Organs	0.0205
Uterus_n	0.0077
	0.0500

Electronic Northern for SEQ. ID NO.: 96

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0027	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0135	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0136	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0010
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0042
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 97

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0077	0.0075	1.0208	0.9796
Small intestine	0.0061	0.0331	0.1854	5.3946
Ovary	0.0030	0.0390	0.0768	13.0292
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0044	0.0154	0.2880	3.4724
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0970	0.0980	10.1999
Heart	0.0000	0.0000	undef	undef
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0789	0.0532	1.4850	0.6734
Stomach-esophagus	0.0290	0.0077	3.7816	0.2644
Muscle-skeleton	0.0027	0.0205	0.1322	7.5658
Kidney	0.0033	0.0055	0.5983	1.6714
Pancreas	0.0120	0.0267	0.4493	2.2259
Penis	0.0153	0.0021	7.1654	0.1396
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0096			
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0445			
Seminal vesicle	0.1411			
Sensory organs	0.0026			
White blood cells	0.1917			
Cervix				

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0061
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0340
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 98

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0056	0.2268	4.4083
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0021	0.0020	1.0161	0.9842
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0027	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0735
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0010
Placenta	Nerves	0.0068
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0083
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 99

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder			
Breast	0.0039	0.0026	1.5254 0.6555
Small intestine	0.0090	0.0056	1.5879 0.6298
Ovary	0.0031	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0156	0.0000 undef
Gastrointestinal	0.0051	0.0025	2.0377 0.4907
Brain	0.0019	0.0046	0.4142 2.4145
Hematopoietic	0.0015	0.0041	0.3600 2.7779
Skin	0.0013	0.0000	undef 0.0000
Hepatic	0.0037	0.0000	undef 0.0000
Heart	0.0000	0.0074	undef undef
Testicles	0.0000	0.0074	undef 0.0000
Lung	0.0000	0.0031	undef undef
Stomach-esophagus	0.0097	0.0000	undef 0.0000
Muscle-skeleton	0.0103	0.0060	1.7133 0.5837
Kidney	0.0081	0.0068	1.1896 0.8406
Pancreas	0.0050	0.0000	undef 0.0000
Penis	0.0090	0.0000	undef 0.0000
Prostate	0.0044	0.0064	0.6824 1.4654
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0051	0.0000	undef 0.0000
Uterus-general	0.0064		
Breast hyperplasia	0.0059		
Prostate hyperplasia	0.0089		
Seminal vesicle	0.0000		
Sensory organs	0.0000		
White blood cells			
Cervix			

FETUS % frequency	
Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Suprarenal gland	0.0036
Kidney	0.0000
Placenta	0.0424
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Breast	0.0204
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0134
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles	0.0000
Lung	0.0164
Nerves	0.0100
Prostate	0.0000
Sensory Organs	0.0077
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 100

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0179	1.7434	0.5736
Breast	0.0205	0.0244	0.8376	1.1939
Small intestine	0.0675	0.0000	undef	0.0000
Ovary	0.0060	0.0442	0.1354	7.3832
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0862	0.0463	1.8638	0.5365
Brain	0.0067	0.0133	0.4984	2.0063
Hematopoietic	0.0120	0.0000	undef	0.0000
Skin	0.0477	0.0000	undef	0.0000
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0212	0.0412	0.5140	1.9456
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0374	0.0450	0.8313	1.2029
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0137	0.0600	0.2284	4.3775
Kidney	0.0054	0.0274	0.1983	5.0439
Pancreas	0.0066	0.0442	0.1496	6.6857
Penis	0.0449	0.0267	1.6847	0.5936
Prostate	0.0240	0.0234	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0136	1.6834	0.5940
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0534			
Sensory organs	0.0235			
White blood cells	0.0303			
Cervix	0.0319			

	FETUS % frequency
Development	
Gastrointestinal	0.0278
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0213
Suprarenal gland	0.0072
Kidney	0.0000
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0304
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles	0.0309
Lung	0.0164
Nerves	0.0020
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 101

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0000	0.0188	0.0000	undef
Ovary	0.0245	0.0000	undef	0.0000
Endocrine tissue	0.0120	0.0442	0.2709	3.6916
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0134	0.0185	0.7248	1.3797
Hematopoietic	0.0007	0.0072	0.1029	9.7228
Skin	0.0321	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0129	0.0000	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0000	0.0234	0.0000	undef
Stomach-esophagus	0.0478	0.0450	1.0623	0.9414
Muscle-skeleton	0.0676	0.0690	0.9804	1.0200
Kidney	0.0069	0.0000	undef	0.0000
Pancreas	0.0000	0.0068	0.0000	undef
Penis	0.0116	0.0055	2.0940	0.4775
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0065	0.0128	0.5118	1.9538
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0235	0.0000	undef
Seminal vesicle	0.1101	0.0000	0.0000	0.0000
Sensory organs	0.0106			
White blood cells				
Cervix				

	FETUS % frequency
Development	
Gastrointestinal	0.0139
Brain	0.0139
Hematopoietic	0.0000
Skin	0.0039
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0229
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0082
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 102

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0588	0.3979	2.5129
Breast	0.0179	0.0507	0.3529	2.8339
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0180	0.0546	0.3289	3.0402
Endocrine tissue	0.0324	0.0251	1.2906	0.7749
Gastrointestinal	0.0364	0.0786	0.4629	2.1603
Brain	0.0067	0.0216	0.3086	3.2409
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0323	0.1471	6.7999
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0270	0.0225	1.2008	0.8328
Stomach-esophagus	0.0290	0.0383	0.7563	1.3222
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0326	0.0616	0.5287	1.8915
Pancreas	0.0132	0.0607	0.2176	4.5964
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0458	0.0617	0.7412	1.3491
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0352			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0356			
Sensory organs	0.0069			
White blood cells	0.0106			
Cervix				

	FETUS % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0167
Hematopoietic	0.0125
Skin	0.0079
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0325
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0303
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0169
Gastrointestinal	0.0488
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0231
Lung	0.0164
Nerves	0.0100
Prostate	0.0205
Sensory Organs	0.0077
Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 103

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0351	0.0256	1.3729	0.7284
Small intestine	0.0077	0.0094	0.8166	1.2245
Ovary	0.0153	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0156	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0211	0.0463	0.4556	2.1950
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0125	0.0204	0.6096	1.6403
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0244	0.0068	3.5687	0.2802
Pancreas	0.0066	0.0110	0.5983	1.6714
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0109	0.0170	0.6398	1.5631
Uterus-endometrium	0.0000	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0954	0.0000	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0272
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0023
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0410
Kidney	Lung	0.0010
Placenta	Nerves	0.0137
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 105

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0230	1.3559	0.7375
Breast	0.0435	0.0320	1.3611	0.7347
Small intestine	0.0429	0.0165	2.5952	0.3853
Ovary	0.0210	0.0676	0.3100	3.2263
Endocrine tissue	0.0341	0.0752	0.4528	2.2083
Gastrointestinal	0.0230	0.0185	1.2425	0.8048
Brain	0.0525	0.0554	0.9466	1.0564
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0330	0.0000	undef	0.0000
Hepatic	0.0143	0.0259	0.5515	1.8133
Heart	0.0329	0.0962	0.3414	2.9288
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0166	0.0327	0.5080	1.9684
Stomach-esophagus	0.0193	0.0307	0.6303	1.5866
Muscle-skeleton	0.0343	0.0240	1.4278	0.7004
Kidney	0.0624	0.0822	0.7600	1.3158
Pancreas	0.0182	0.0055	3.2906	0.3039
Penis	0.0419	0.0000	undef	0.0000
Prostate	0.0174	0.0405	0.4310	2.3202
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0381	0.0136	2.8057	0.3564
Uterus-general	0.0662	0.0954	0.6939	1.4412
Breast hyperplasia	0.0608			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0623			
Sensory organs	0.0235			
White blood cells	0.0035			
Cervix	0.0213			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0490
Skin	Fetal	0.0047
Hepatic	Gastrointestinal	0.0488
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0356
Suprarenal gland	Testicles	0.0154
Kidney	Lung	0.0410
Placenta	Nerves	0.0402
Prostate	Prostate	0.0205
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0375

Electronic Northern for SEQ. ID NO.: 106

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0639	0.3051	3.2777
Breast	0.0333	0.0470	0.7077	1.4129
Small intestine	0.0399	0.1819	0.2191	4.5647
Ovary	0.0150	0.0702	0.2132	4.6905
Endocrine tissue	0.0238	0.0903	0.2642	3.7857
Gastrointestinal	0.0900	0.1110	0.8111	1.2329
Brain	0.0067	0.0267	0.2492	4.0126
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0143	0.0323	0.4412	2.2666
Heart	0.0011	0.0962	0.0110	90.7941
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0062	0.0184	0.3387	2.9526
Stomach-esophagus	0.0000	0.3527	0.1370	7.2985
Muscle-skeleton	0.0733	0.0360	0.0000	undef
Kidney	0.0694	0.0276	2.5128	0.3980
Pancreas	0.0090	0.0533	0.1685	5.9357
Penis	0.0109	0.0255	0.4265	2.3446
Prostate	0.0270	0.0000	undef	0.0000
Uterus-endometrium	0.0076	0.0272	0.2806	3.5642
Uterus-myometrium	0.0000	0.4771	0.0000	undef
Uterus-general	0.0576			
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.1068			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0061			
Sensory organs	0.0319			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0813	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.4149
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0145	Skin-muscle	0.0154
Suprarenal gland	0.0000	Testicles	0.0573
Kidney	0.0309	Lung	0.0040
Placenta	0.0121	Nerves	0.0068
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 107

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder			
Breast	0.0078	0.0204	0.3814 2.6222
Small intestine	0.0102	0.0132	0.7777 1.2858
Ovary	0.0153	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0208	0.0000 undef
Gastrointestinal	0.0119	0.0075	1.5849 0.6309
Brain	0.0307	0.0093	3.3134 0.3018
Hematopoietic	0.0111	0.0144	0.7714 1.2964
Skin	0.0094	0.0379	0.2470 4.0483
Hepatic	0.0441	0.0000	undef 0.0000
Heart	0.0095	0.0000	undef 0.0000
Testicles	0.0170	0.0000	undef 0.0000
Lung	0.0058	0.0000	undef 0.0000
Stomach-esophagus	0.0229	0.0245	0.9314 1.0737
Muscle-skeleton	0.0097	0.0000	undef 0.0000
Kidney	0.0034	0.0120	0.2856 3.5020
Pancreas	0.0190	0.0205	0.9252 1.0808
Penis	0.0083	0.0110	0.7479 1.3371
Prostate	0.0030	0.0267	0.1123 8.9035
Uterus-endometrium	0.0065	0.0106	0.6142 1.6282
Uterus-myometrium	0.0405	0.0000	undef 0.0000
Uterus-general	0.0000	0.0272	0.0000 undef
Breast hyperplasia	0.0096	0.0000	undef undef
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0191		
Sensory organs	0.0106		
White blood cells			
Cervix			

FETUS % frequency	
Development	
Gastrointestinal	0.0278
Brain	0.0083
Hematopoietic	0.0188
Skin	0.0079
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0072
Suprarenal gland	0.0072
Kidney	0.0254
Placenta	0.0185
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles	0.0000
Lung	0.0082
Nerves	0.0131
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 108

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0051	0.0132	0.3889	2.5715
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0034	0.0125	0.2717	3.6805
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0093	0.0123	0.7621	1.3122
Stomach-esophagus	0.0034	0.0153	0.6303	1.5866
Muscle-skeleton	0.0027	0.0068	0.3965	2.5219
Kidney	0.0017	0.0055	0.2991	3.3428
Pancreas	0.0090	0.0267	0.3369	2.9678
Penis	0.0392	0.0213	1.8425	0.5427
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0238			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0104			
White blood cells	0.0106			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0105
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0285
Lung	Skin-muscle	0.0324
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0246
Placenta	Nerves	0.0020
Prostate	Prostate	0.0410
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 110

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0102	0.7627	1.3111
Small intestine	0.0166	0.0282	0.5898	1.6955
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0390	0.1535	6.5146
Gastrointestinal	0.0392	0.0527	0.7439	1.3442
Brain	0.0153	0.0370	0.4142	2.4145
Hematopoietic	0.0059	0.0072	0.8228	1.2153
Skin	0.0080	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0129	0.0000	undef
Testicles	0.0064	0.0687	0.0925	10.8088
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0239	0.0470	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0120	0.0120	0.9994	1.0006
Pancreas	0.0299	0.0000	undef	0.0000
Penis	0.0182	0.0110	1.6453	0.6078
Prostate	0.0210	0.0000	undef	0.0000
Uterus-endometrium	0.0203	0.1055	0.1920	5.2070
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0352			
Prostate hyperplasia	0.0446			
Seminal vesicle	0.0267			
Sensory organs	0.0353			
White blood cells	0.0147			
Cervix	0.0106			

FETUS	% frequency
Development	
Gastrointestinal	0.0000
Brain	0.0222
Hematopoietic	0.0000
Skin	0.0197
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0178
Suprarenal gland	0.0000
Kidney	0.0145
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0068
Ovary_n	0.1595
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0408
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles	0.0000
Lung	0.0410
Nerves	0.0151
Prostate	0.0342
Sensory Organs	0.0155
Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 111

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0117	0.0460	0.2542	3.9333
Small intestine	0.0192	0.0376	0.5104	1.9593
Ovary	0.0000	0.0496	0.0000	undef
Endocrine tissue	0.0030	0.0234	0.1279	7.8175
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0007	0.0000	undef	0.0000
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0147	0.0000	undef	0.0000
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0062	0.0102	0.6096	1.6403
Muscle-skeleton	0.0193	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0271	0.0137	1.9826	0.5044
Penis	0.0132	0.0221	0.5983	1.6714
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0240	0.0298	0.8043	1.2434
Uterus-myometrium	0.0000	0.0528	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0352	0.0954	0.0000	undef
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0106			

	FETUS % frequency
Development	
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0408
Ovary_n	0.0000
Ovary_t	0.0608
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0246
Nerves	0.0000
Prostate	0.0205
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 112

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0051	0.7627	1.3111
Small intestine	0.0051	0.0207	0.2475	4.0410
Ovary	0.0123	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0338	0.0886	11.2920
Gastrointestinal	0.0017	0.0025	0.6792	1.4722
Brain	0.0038	0.0185	0.2071	4.8289
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0847	0.0433	23.0839
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0275	0.1927	5.1882
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0109	0.0000	undef	0.0000
Kidney	0.0033	0.0055	0.5983	1.6714
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0044	0.0000	undef	0.0000
Prostate	0.0135	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0213			
Cervix				

STANDARDIZED/SUBTRACTED	
FETUS	LIBRARIES
% frequency	% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0354
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0071	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0062	Nerves	0.0000
Prostate	0.0000	Prostate	0.0155
Sensory organs	0.0249	Sensory Organs	0.0375
	0.0251	Uterus_n	

Electronic Northern for SEQ. ID NO.: 113

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0117	0.0409	0.2860 3.4963
Breast	0.0256	0.0376	0.6805 1.4694
Small intestine	0.0399	0.0000	undef 0.0000
Ovary	0.0090	0.0390	0.2303 4.3431
Endocrine tissue	0.0477	0.0702	0.6792 1.4722
Gastrointestinal	0.0479	0.0231	2.0708 0.4829
Brain	0.0229	0.0349	0.6564 1.5234
Hematopoietic	0.0281	0.0000	undef 0.0000
Skin	0.0624	0.0000	undef 0.0000
Hepatic	0.0048	0.0259	0.1838 5.4400
Heart	0.0519	0.0000	undef 0.0000
Testicles	0.0230	0.0468	0.4920 2.0326
Lung	0.0270	0.0491	0.5504 1.8170
Stomach-esophagus	0.0387	0.0230	1.6807 0.5950
Muscle-skeleton	0.0377	0.0840	0.4487 2.2286
Kidney	0.0462	0.0411	1.1235 0.8901
Pancreas	0.0116	0.0276	0.4188 2.3877
Penis	0.0150	0.0533	0.2808 3.5614
Prostate	0.0283	0.0490	0.5786 1.7284
Uterus-endometrium	0.0541	0.0528	1.0243 0.9763
Uterus-myometrium	0.0305	0.0272	1.1223 0.8911
Uterus-general	0.0255	0.0000	undef 0.0000
Breast hyperplasia	0.0192		
Prostate hyperplasia	0.0386		
Seminal vesicle	0.0267		
Sensory organs	0.0353		
White blood cells	0.0312		
Cervix	0.0213		

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.1595
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0164
Kidney	Lung 0.0050
Placenta	Nerves 0.0068
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 115

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0051	0.7627 1.3111
Breast	0.0000	0.0000	undef undef
Small intestine	0.0061	0.0000	undef 0.0000
Ovary	0.0000	0.0702	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0192	0.0185	1.0354 0.9658
Brain	0.0007	0.0000	undef 0.0000
Hematopoietic	0.0053	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0058	0.0000	undef 0.0000
Testicles	0.0052	0.0020	2.5402 0.3937
Lung	0.0193	0.0230	0.8404 1.1900
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0017	0.0110	0.1496 6.6857
Pancreas	0.0000	0.0000	undef undef
Penis	0.0065	0.0000	undef 0.0000
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0954	0.0000 undef
Uterus-myometrium	0.0000		
Uterus-general	0.0000		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0118		
Seminal vesicle	0.0000		
Sensory organs	0.0000		
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0101
Hematopoietic	0.0000
Skin	0.0047
Hepatic	0.0122
Heart-blood vessels	0.0114
Lung	0.0065
Suprarenal gland	0.0000
Kidney	0.0010
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0167
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0068
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 116

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0026	0.0000 undef
Breast	0.0038	0.0038	1.0208 0.9796
Small intestine	0.0061	0.0165	0.3707 2.6973
Ovary	0.0030	0.0208	0.1439 6.9489
Endocrine tissue	0.0102	0.0025	4.0755 0.2454
Gastrointestinal	0.0057	0.0046	1.2425 0.8048
Brain	0.0030	0.0031	0.9599 1.0417
Hematopoietic	0.0094	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0095	0.0000	undef 0.0000
Heart	0.0058	0.0000	undef 0.0000
Testicles	0.0073	0.0123	0.5927 1.6872
Lung	0.0000	0.0077	0.0000 undef
Stomach-esophagus	0.0051	0.0000	undef 0.0000
Muscle-skeleton	0.0081	0.0068	1.1896 0.8406
Kidney	0.0017	0.0055	0.2991 3.3428
Pancreas	0.0000	0.0000	undef undef
Penis	0.0065	0.0021	3.0709 0.3256
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0064		
Uterus-general	0.0000		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0078		
Seminal vesicle	0.0000		
Sensory organs			
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0036
Lung	0.0036
Suprarenal gland	0.0254
Kidney	0.0124
Placenta	0.0000
Prostate	0.0249
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0032
Skin-muscle	0.0154
Testicles	0.0082
Lung	0.0060
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0208
Uterus_n	

Electronic Northern for SEQ. ID NO.: 117

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0517	0.0879	0.5886	1.6991
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0381	0.0518	0.7353	1.3600
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0164	0.0635	15.7470
Lung	0.0290	0.0230	1.2605	0.7933
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0033	0.0110	undef	undef
Kidney	0.0000	0.0000	0.2991	3.3428
Pancreas	0.0022	0.0043	0.5118	1.9538
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0051
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 120

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0000	0.0026	0.0000 undef
Breast	0.0013	0.0056	0.2268 4.4083
Small intestine	0.0031	0.0000	undef 0.0000
Ovary	0.0000	0.0156	0.0000 undef
Endocrine tissue	0.0019	0.0046	undef undef
Gastrointestinal	0.0022	0.0031	0.4142 2.4145
Brain	0.0040	0.0000	undef 0.0000
Hematopoietic	0.0073	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0042	0.0000	undef 0.0000
Heart	0.0058	0.0000	undef 0.0000
Testicles	0.0010	0.0061	0.1693 5.9051
Lung	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0017	0.0000	undef 0.0000
Muscle-skeleton	0.0027	0.0068	0.3965 2.5219
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0022	0.0021	1.0236 0.9769
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0051	0.0000	0.0000 undef
Uterus-myometrium	0.0032		undef 0.0000
Uterus-general	0.0030		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0043		
Seminal vesicle	0.0000		
Sensory organs			
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0023
Hepatic	Gastrointestinal	0.0114
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0082
Kidney	Lung	0.0000
Placenta	Nerves	0.0068
Prostate	Prostate	0.0155
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 121

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0117	0.0153	0.7627 1.3111
Breast	0.0026	0.0132	0.1944 5.1431
Small intestine	0.0031	0.0165	0.1854 5.3946
Ovary	0.0000	0.0156	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0019	0.0046	0.4142 2.4145
Brain	0.0030	0.0062	0.4800 2.0835
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.1760	0.0518	3.4008 0.2941
Heart	0.0021	0.0000	undef 0.0000
Testicles	0.0058	0.0117	0.4920 2.0326
Lung	0.0010	0.0082	0.1270 7.8735
Stomach-esophagus	0.0000	0.0077	0.0000 undef
Muscle-skeleton	0.0188	0.0060	3.1411 0.3184
Kidney	0.0081	0.0000	undef 0.0000
Pancreas	0.0033	0.0000	undef 0.0000
Penis	0.0000	0.0277	0.6299 1.5875
Prostate	0.0174	0.0528	0.0000 undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0000	0.0954	0.0000 undef
Uterus-general	0.0032		
Breast hyperplasia	0.0119		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0235		
Sensory organs	0.0009		
White blood cells	0.0000		
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0203
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0010
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 122

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.1053	0.1125	0.9361 1.0683
Breast	0.1164	0.1015	1.1468 0.8720
Small intestine	0.0491	0.0662	0.7415 1.3487
Ovary	0.0479	0.1015	0.4723 2.1173
Endocrine tissue	0.0562	0.0251	2.2415 0.4461
Gastrointestinal	0.1015	0.1758	0.5777 1.7311
Brain	0.0296	0.1273	0.2322 4.3058
Hematopoietic	0.0535	0.0000	undef 0.0000
Skin	0.2166	0.0000	undef 0.0000
Hepatic	0.0809	0.1035	0.7813 1.2800
Heart	0.4133	0.2612	1.5825 0.6319
Testicles	0.0748	0.0468	1.5989 0.6254
Lung	0.1506	0.1227	1.2278 0.8145
Stomach-esophagus	0.2126	0.1073	1.9808 0.5048
Muscle-skeleton	0.0805	0.1680	0.4793 2.0863
Kidney	0.0543	0.0890	0.6100 1.6393
Pancreas	0.0562	0.1712	0.3281 3.0479
Penis	0.1497	0.2399	0.6240 1.6026
Prostate	0.0850	0.0362	2.3483 0.4258
Uterus-endometrium	0.0541	0.0000	undef 0.0000
Uterus-myometrium	0.0457	0.1019	0.4489 2.2276
Uterus-general	0.0560	0.0000	undef 0.0000
Breast hyperplasia	0.0991		
Prostate hyperplasia	0.0832		
Seminal vesicle	0.0801		
Sensory organs	0.1059		
White blood cells	0.0720		
Cervix	0.0639		

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0835
Gastrointestinal	0.0361
Brain	0.0063
Hematopoietic	0.0433
Skin	0.0000
Hepatic	0.0961
Heart-blood vessels	0.0867
Lung	0.0761
Suprarenal gland	0.0309
Kidney	0.1151
Placenta	0.5984
Prostate	0.0251
Sensory organs	
Breast	0.0544
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0466
Gastrointestinal	0.0610
Hematopoietic	0.0000
Skin-muscle	0.0421
Testicles	0.0000
Lung	0.1474
Nerves	0.0110
Prostate	0.0205
Sensory Organs.	0.0000
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 123

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0039	0.0026	1.5254 0.6555
Breast	0.0013	0.0019	0.6805 1.4694
Small intestine	0.0061	0.0000	undef 0.0000
Ovary	0.0000	0.0182	0.0000 undef
Endocrine tissue	0.0017	0.0075	0.2264 4.4166
Gastrointestinal	0.0000	0.0093	0.0000 undef
Brain	0.0030	0.0021	1.4399 0.6945
Hematopoietic	0.0013	0.0000	undef 0.0000
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0053	0.0000	undef 0.0000
Testicles	0.0115	0.0000	undef 0.0000
Lung	0.0010	0.0061	0.1693 5.9051
Stomach-esophagus	0.0000	0.0077	0.0000 undef
Muscle-skeleton	0.0086	0.0060	1.4278 0.7004
Kidney	0.0027	0.0205	0.1322 7.5658
Pancreas	0.0066	0.0055	1.1966 0.8357
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0044	0.0021	2.0473 0.4885
Uterus-endometrium	0.0068	0.0000	undef 0.0000
Uterus-myometrium	0.0076	0.0068	1.1223 0.8911
Uterus-general	0.0000	0.0000	undef undef
Breast hyperplasia	0.0064		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs			
White blood cells			
Cervix			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0254
Suprarenal gland	0.0062
Kidney	0.0182
Placenta	0.0000
Prostate	0.0000
Sensory organs	
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0134
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0130
Skin-muscle	0.0000
Testicles	0.0164
Lung	0.0030
Nerves	0.0000
Prostate	0.0125
Sensory Organs	
Uterus_n	

Electronic Northern for Seq. ID: 258

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0047	0.0000 undef
Breast	0.0018	0.0014	1.2524 0.7985
Large intestine	0.0019	0.0000	undef 0.0000
Small intestine	0.0027	0.0213	0.1288 7.7625
Ovary	0.0000	0.0167	0.0000 undef
Endocrine tissue	0.0064	0.0000	undef 0.0000
Brain	0.0012	0.0010	1.1605 0.8617
Skin	0.0000	0.0000	undef undef
Hepatic	0.0051	0.0000	undef undef
Heart	0.0080	0.0118	0.6786 1.4737
Testicles	0.0029	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0037	0.0000 undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0017	0.0000	undef 0.0000
Pancreas	0.0019	0.0000	undef 0.0000
Prostate	0.0025	0.0000	undef 0.0000
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0040	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Seminal vesicle	0.0000	0.0000	undef undef
Sensory organs	0.0000	0.0000	undef undef

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0098
Lungs_n	0.0000
Lungs_t	0.0030
Nerves	0.0000
Kidney_t	0.0000
Ovary_Uterus	0.0121
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 259

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0117	0.0023	4.9785 0.2009
Breast	0.0070	0.0014	5.0097 0.1996
Large intestine	0.0000	0.0057	0.0000 undef
Small intestine	0.0082	0.0000	undef 0.0000
Ovary	0.0000	0.0119	0.0000 undef
Endocrine tissue	0.0032	0.0089	0.3621 2.7613
Brain	0.0006	0.0000	undef 0.0000
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0081	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0145	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0037	0.0000 undef
Muscle-skeleton	0.0022	0.0000	undef 0.0000
Kidney	0.0017	0.0000	undef 0.0000
Pancreas	0.0019	0.0000	undef 0.0000
Prostate	0.0025	0.0075	0.3381 2.9576
T lymphoma	0.0059	0.0138	0.4284 2.3344
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0027		
Hematopoietic	0.0080		
Penis	0.0141		
Seminal vesicle	0.0000		
Sensory organs			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0071
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0062
Kidney	0.0061
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0245
Endocrine tissue	0.0070
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0084
Testicles_n	0.0000
Testicles_t	0.0195
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary_Uterus	0.0061
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 260

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0000	0.0000	undef undef
Breast	0.0000	0.0023	0.0000 undef
Large intestine	0.0062	0.0000	undef 0.0000
Small intestine	0.0019	0.0085	0.2243 4.4591
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0525	0.0000 undef
Brain	0.0032	0.0071	0.4527 2.2091
Skin	0.0023	0.0020	1.1605 0.8617
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0063	0.0000 undef
Testicles	0.0051	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0088	0.0037	2.3680 0.4223
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0017	0.0000	undef 0.0000
Pancreas	0.0022	0.0000	undef 0.0000
Prostate	0.0083	0.0000	undef 0.0000
T lymphoma	0.0028	0.0013	2.1706 0.4607
Uterus	0.0051	0.0224	0.2254 4.4364
White blood cells	0.0015	0.0000	undef 0.0000
Hematopoietic	0.0027	0.0304	0.0902 11.0896
Penis	0.0013		
Seminal vesicle	0.0000		
Sensory organs	0.0070		

FETUS
% freq.

Development	
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0098
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0060
Nerves	0.0000
Kidney_t	0.0113
Ovary_Uterus	0.0000
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 261

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0000	undef 0.0000
Breast	0.0000	0.0000	undef undef
Large intestine	0.0009	0.0014	0.6262 1.5969
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0027	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0191	0.0000 undef
Brain	0.0000	0.0000	undef undef
Skin	0.0006	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0010	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0019	0.0000	0.0000 undef
T lymphoma	0.0051	0.0000	undef 0.0000
Uterus	0.0015	0.0000	undef 0.0000
White blood cells	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0013		
Penis	0.0000		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0168
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0023
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0023
Ovary_Uterus	0.0061
Prostate_n	0.0000
Sensory_Organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 262

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0150	0.0000	undef 0.0000
Breast	0.0156	0.0023	6.6380 0.1506
Large intestine	0.0158	0.0056	2.8179 0.3549
Small intestine	0.0038	0.0028	1.3456 0.7432
Ovary	0.0110	0.0320	0.3435 2.9109
Endocrine tissue	0.0178	0.0334	0.5333 1.8752
Brain	0.0064	0.0213	0.3018 3.3136
Skin	0.0081	0.0060	1.3539 0.7386
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0139	0.0190	0.7324 1.3653
Testicles	0.0193	0.0000	undef 0.0000
Lung	0.0080	0.0118	0.6786 1.4737
Stomach-esophagus	0.0175	0.0129	1.3531 0.7390
Muscle-skeleton	0.0000	0.0064	0.0000 undef
Kidney	0.0017	0.0111	0.1546 6.4671
Pancreas	0.0045	0.0096	0.4642 2.1540
Prostate	0.0132	0.0000	undef 0.0000
T lymphoma	0.0104	0.0091	1.1370 0.8795
Uterus	0.0101	0.0149	0.6762 1.4788
White blood cells	0.0192	0.0230	0.8353 1.1971
Hematopoietic	0.0055	0.0304	0.1803 5.5448
Penis	0.0067		
Seminal vesicle	0.0080		
Sensory organs	0.0070		
	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0275
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0000
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0203
Endocrine tissue	0.0000
Fetal	0.0162
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0454
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0100
Kidney_t	0.0000
Ovary_Uterus	0.0293
Prostate_n	0.0000
Sensory_Organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 263

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0125	0.0136	0.9198 1.0872
Breast	0.0039	0.0188	0.2075 4.8204
Large intestine	0.0114	0.0281	0.4070 2.4568
Small intestine	0.0211	0.0142	1.4801 0.6756
Ovary	0.0082	0.0000	undef 0.0000
Endocrine tissue	0.0089	0.0286	0.3111 3.2147
Brain	0.0161	0.0151	1.0599 0.9435
Skin	0.0211	0.0110	1.9234 0.5199
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0046	0.0127	0.3662 2.7307
Testicles	0.0162	0.0000	undef 0.0000
Lung	0.0080	0.0178	0.4523 2.2108
Stomach-esophagus	0.0136	0.0111	1.2278 0.8145
Muscle-skeleton	0.0072	0.0128	0.5666 1.7648
Kidney	0.0158	0.0185	1.0206 0.9799
Pancreas	0.0157	0.0145	1.0831 0.9232
Prostate	0.0083	0.0221	0.3739 2.6743
T lymphoma	0.0123	0.0039	3.1352 0.3190
Uterus	0.0000	0.0149	0.0000 undef
White blood cells	0.0077	0.0230	0.3368 2.9694
Hematopoietic	0.0082	0.0000	undef 0.0000
Penis	0.0094		
Seminal vesicle	0.0107		
Sensory organs	0.0070		
	0.0235		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0107
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0203
Endocrine tissue	0.0069
Fetal	0.0488
Gastrointestinal	0.0000
Hematopoietic	0.0032
Skin-muscle	0.0167
Testicles_n	0.0000
Testicles_t	0.0195
Lungs_n	0.0000
Lungs_t	0.0060
Nerves	0.0000
Kidney_t	0.0158
Ovary_Uterus	0.0061
Prostate_n	0.0000
Sensory_Organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 264

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0150	0.0136	1.1037 0.9060
Large intestine	0.0273	0.0211	1.2907 0.7748
Small intestine	0.0229	0.0632	0.3618 2.7639
Ovary	0.0268	0.0256	1.0466 0.9555
Endocrine tissue	0.0192	0.0000	undef 0.0000
Brain	0.0089	0.0501	0.1778 5.6255
Skin	0.0193	0.0142	1.3580 0.7364
Hepatic	0.0041	0.0160	0.2539 3.9391
Heart	0.0073	0.0000	undef 0.0000
Testicles	0.0465	0.0254	1.8311 0.5461
Lung	0.0091	0.0412	0.2215 4.5144
Stomach-esophagus	0.0120	0.0000	undef 0.0000
Muscle-skeleton	0.0204	0.0185	1.1050 0.9049
Kidney	0.0290	0.0384	0.7557 1.3233
Pancreas	0.0069	0.0185	0.3711 2.6946
Prostate	0.0537	0.0289	1.8570 0.5385
T lymphoma	0.0380	0.0110	3.4403 0.2907
Uterus	0.0330	0.0130	2.5323 0.3949
White blood cells	0.0051	0.0075	0.6762 1.4788
Hematopoietic	0.0148	0.0138	1.0709 0.9338
Penis	0.0075	0.0000	undef 0.0000
Seminal vesicle	0.0147		
Sensory organs	0.0054		
	0.0000		
	0.0235		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0062
Kidney	0.0121
Placenta	0.0249
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0040
Nerves	0.0000
Kidney_t	0.0090
Ovary_Uterus	0.0121
Prostate_n	0.0000
Sensory_Organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 265

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0000	0.0272	0.0000 undef
Breast	0.0117	0.0023	4.9785 0.2009
Large intestine	0.0141	0.0155	0.9109 1.0979
Small intestine	0.0920	0.0968	0.9498 1.0528
Ovary	0.0247	0.0000	undef 0.0000
Endocrine tissue	0.0208	0.0882	0.2354 4.2478
Brain	0.0016	0.0000	undef 0.0000
Skin	0.0000	0.0010	0.0000 undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0444	0.0000 undef
Testicles	0.0000	0.0000	undef undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0165	0.0111	1.4909 0.6707
Muscle-skeleton	0.0362	0.0128	2.8338 0.3529
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0000	0.0166	0.0000 undef
T lymphoma	0.0207	0.0352	0.5895 1.6963
Uterus	0.0025	0.0000	undef 0.0000
White blood cells	0.0030	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0000		
Seminal vesicle	0.0915		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0278
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0108
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0253
Ovary_t	0.0000
Endocrine tissue	0.0023
Fetal	0.0244
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0084
Testicles_n	0.0000
Testicles_t	0.0293
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0113
Ovary_Uterus	0.0182
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 266

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0000	undef 0.0000
Breast	0.0000	0.0000	undef undef
Large intestine	0.0114	0.0000	undef 0.0000
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0055	0.0000	undef 0.0000
Endocrine tissue	0.0059	0.0525	0.1131 8.8401
Brain	0.0161	0.0035	4.5268 0.2209
Skin	0.0017	0.0000	undef 0.0000
Hepatic	0.0073	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0071	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0049	0.0037	1.3155 0.7601
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0017	0.0000	undef 0.0000
Pancreas	0.0470	0.0048	9.7491 0.1026
Prostate	0.0033	0.0000	undef 0.0000
T lymphoma	0.0019	0.0000	undef 0.0000
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0044	0.0046	0.9638 1.0375
Hematopoietic	0.0007	0.0000	undef 0.0000
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0020
Nerves	0.0000
Kidney_t	0.0023
Ovary_Uterus	0.0000
Prostate_n	0.0000
Sensory_organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 267

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0000	0.0070	0.0000 undef
Breast	0.0026	0.0014	1.8786 0.5323
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0000	0.0119	0.0000 undef
Endocrine tissue	0.0034	0.0010	2.9013 0.3447
Brain	0.0000	0.0394	0.0000 undef
Skin	0.0040	0.0000	undef undef
Hepatic	0.0000	0.0000	undef 0.0000
Heart	0.0030	0.0000	undef undef
Testicles	0.0000	0.0000	undef 0.0000
Lung	0.0007	0.0000	undef undef
Stomach-esophagus	0.0049	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0034	0.0000	undef 0.0000
Pancreas	0.0000	0.0048	undef 0.0000
Prostate	0.0000	0.0000	0.0000 undef
T lymphoma	0.0028	0.0000	undef undef
Uterus	0.0000	0.0000	undef 0.0000
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0007	0.0000	undef undef
Penis	0.0000	0.0000	undef 0.0000
Seminal vesicle	0.0054		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney_t	0.0000
Ovary_Uterus	0.0023
Prostate_n	0.0000
Sensory_Organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 268

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0000	undef 0.0000
Breast	0.0117	0.0094	1.2446 0.9035
Large intestine	0.0088	0.0253	0.3479 2.8744
Small intestine	0.0192	0.0028	6.7278 0.1486
Ovary	0.0192	0.0213	0.9018 1.1089
Endocrine tissue	0.0030	0.0143	0.2074 4.8219
Brain	0.0193	0.0035	5.4321 0.1841
Skin	0.0081	0.0249	0.3249 3.0774
Hepatic	0.0184	0.0000	undef 0.0000
Heart	0.0093	0.0063	1.4649 0.6826
Testicles	0.0112	0.0000	undef 0.0000
Lung	0.0040	0.0118	0.3393 2.9475
Stomach-esophagus	0.0126	0.0037	3.4204 0.2924
Muscle-skeleton	0.0072	0.0000	undef 0.0000
Kidney	0.0120	0.0037	3.2472 0.3080
Pancreas	0.0157	0.0048	3.2497 0.3077
Prostate	0.0050	0.0110	0.4487 2.2285
T lymphoma	0.0104	0.0052	1.9897 0.5026
Uterus	0.0051	0.0000	undef 0.0000
White blood cells	0.0163	0.0092	1.7670 0.5659
Hematopoietic	0.0110	0.0000	undef 0.0000
Penis	0.0027		
Seminal vesicle	0.0054		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0257
Skin-muscle	0.0032
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0010
Nerves	0.0000
Kidney_t	0.0023
Ovary_Uterus	0.0243
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 269

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0156	0.0047	3.3190 0.3013
Breast	0.0079	0.0014	5.6359 0.1774
Large intestine	0.0096	0.0057	1.6820 0.5945
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0030	0.0191	0.1555 6.4291
Endocrine tissue	0.0064	0.0018	3.6214 0.2761
Brain	0.0058	0.0060	0.9671 1.0340
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0091	0.0000	undef 0.0000
Testicles	0.0080	0.0000	undef 0.0000
Lung	0.0068	0.0037	1.8417 0.5430
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0034	0.0111	0.3093 3.2335
Kidney	0.0045	0.0000	undef 0.0000
Pancreas	0.0083	0.0110	0.7479 1.3371
Prostate	0.0057	0.0117	0.4823 2.0732
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0044	0.0092	0.4819 2.0750
White blood cells	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0027		
Penis	0.0188		
Seminal vesicle	0.0141		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0152
Ovary_t	0.0000
Endocrine tissue	0.0006
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0032
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0020
Nerves	0.0000
Kidney_t	0.0068
Ovary_Uterus	0.0000
Prostate_n	0.0077
Sensory_organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 270

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0156	0.0047	3.3190 0.3013
Breast	0.0167	0.0197	0.8499 1.1767
Large intestine	0.0167	0.0199	1.5378 0.6503
Small intestine	0.0307	0.0213	0.3865 2.5875
Ovary	0.0082	0.0334	0.1778 5.6255
Endocrine tissue	0.0059	0.0248	1.2934 0.7732
Brain	0.0321	0.0170	2.1504 0.4650
Skin	0.0365	0.0000	undef 0.0000
Hepatic	0.0257	0.0127	0.0000 undef
Heart	0.0000	0.0000	undef 0.0000
Testicles	0.0426	0.0000	undef 0.0000
Lung	0.0161	0.0118	1.3571 0.7369
Stomach-esophagus	0.0272	0.0222	1.2278 0.8144
Muscle-skeleton	0.0072	0.0000	undef 0.0000
Kidney	0.0137	0.0074	1.8555 0.5389
Pancreas	0.0246	0.0145	1.7022 0.5875
Prostate	0.0050	0.0000	undef 0.0000
T lymphoma	0.0179	0.0065	2.7494 0.3637
Uterus	0.0177	0.0672	0.2630 3.8026
White blood cells	0.0118	0.0046	2.5703 0.3891
Hematopoietic	0.0219	0.0000	undef 0.0000
Penis	0.0188		
Seminal vesicle	0.0281		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0108
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0110
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0281
Kidney_t	0.0000
Ovary_Uterus	0.0068
Prostate_n	0.0061
Sensory organs	0.0232
White blood cells	0.0000

Electronic Northern for Seq. ID: 271

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0125	0.0407	0.3066 3.2617
Breast	0.0117	0.0164	0.7112 1.4061
Large intestine	0.0123	0.0098	1.2524 0.7985
Small intestine	0.0057	0.0057	1.0092 0.9909
Ovary	0.0165	0.0000	undef 0.0000
Endocrine tissue	0.0030	0.0143	0.2074 4.8219
Brain	0.0096	0.0195	0.4938 2.0250
Skin	0.0122	0.0070	1.7408 0.5745
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0093	0.0000	undef 0.0000
Testicles	0.0071	0.0137	0.5169 1.9347
Lung	0.0201	0.0059	3.3928 0.2947
Stomach-esophagus	0.0117	0.0148	0.7893 1.2669
Muscle-skeleton	0.0072	0.0320	0.2267 4.4110
Kidney	0.0086	0.0000	undef 0.0000
Pancreas	0.0045	0.0096	0.4642 2.1540
Prostate	0.0017	0.0055	0.2992 3.3427
T lymphoma	0.0066	0.0117	0.5627 1.7770
Uterus	0.0126	0.0149	0.8453 1.1830
White blood cells	0.0062	0.0322	0.1836 5.4469
Hematopoietic	0.0107	0.0304	0.2029 4.9287
Penis	0.0000		
Seminal vesicle	0.0141		
Sensory organs	0.0235		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0250
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0220
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0421
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0211
Nerves	0.0000
Kidney_t	0.0248
Ovary_Uterus	0.0000
Prostate_n	0.0232
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 272

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0136	0.1840 5.4361
Breast	0.0039	0.0117	0.3319 3.0130
Large intestine	0.0246	0.0070	3.5068 0.2852
Small intestine	0.0287	0.0399	0.7208 1.3873
Ovary	0.0082	0.0426	0.1932 5.1750
Endocrine tissue	0.0148	0.0381	0.3889 2.5717
Brain	0.0161	0.0266	0.6036 1.6568
Skin	0.0220	0.0130	1.6961 0.5896
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0000	0.0381	0.0000 undef
Testicles	0.0132	0.0000	undef 0.0000
Lung	0.0040	0.0000	undef 0.0000
Stomach-esophagus	0.0214	0.0129	1.6538 0.6047
Muscle-skeleton	0.0000	0.0064	0.0000 undef
Kidney	0.0069	0.0000	undef 0.0000
Pancreas	0.0134	0.0193	0.6964 1.4360
Prostate	0.0264	0.0276	0.9573 1.0446
T lymphoma	0.0075	0.0104	0.7235 1.3821
Uterus	0.0227	0.0373	0.6086 1.6431
White blood cells	0.0059	0.0138	0.4284 2.3344
Hematopoietic	0.0082	0.0607	0.1353 7.3931
Penis	0.0053		
Seminal vesicle	0.0161		
Sensory organs	0.0141		

FETUS
% freq.

Development	0.0278
Gastrointestinal	0.0056
Brain	0.0375
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0036
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0061
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0195
Lungs_n	0.0000
Lungs_t	0.0121
Nerves	0.0000
Kidney_t	0.0000
Ovary_Uterus	0.0061
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 273

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0000	undef 0.0000
Breast	0.0078	0.0188	0.4149 2.4104
Large intestine	0.0079	0.0112	0.7045 1.4195
Small intestine	0.0019	0.0057	0.3364 2.9727
Ovary	0.0055	0.0000	undef 0.0000
Endocrine tissue	0.0030	0.0215	0.1383 7.2328
Brain	0.0080	0.0053	1.5089 0.6627
Skin	0.0041	0.0070	0.5803 1.7234
Hepatic	0.0147	0.0000	undef 0.0000
Heart	0.0046	0.0000	undef 0.0000
Testicles	0.0203	0.0000	undef 0.0000
Lung	0.0000	0.0355	0.0000 undef
Stomach-esophagus	0.0039	0.0111	0.3508 2.8506
Muscle-skeleton	0.0145	0.0128	1.1335 0.8822
Kidney	0.0120	0.0074	1.6236 0.6159
Pancreas	0.0000	0.0048	0.0000 undef
Prostate	0.0085	0.0065	1.3023 0.7679
T lymphoma	0.0303	0.0149	2.0287 0.4929
Uterus	0.0133	0.0092	1.4458 0.6917
White blood cells	0.0205	0.0000	undef 0.0000
Hematopoietic	0.0027		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0213
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0152
Fetal	0.0245
Gastrointestinal	0.0023
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0060
Kidney_t	0.0000
Ovary_Uterus	0.0090
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

2.2. Fisher Test

In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S. If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

The consensus sequence C will generally be longer than initial sequence S. Its electronic Northern Blot will

accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i : iteration index) obtained in each case until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from ovarian tumor tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

Example 4**Mapping of nucleic acid sequences on the human genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the gap between genome mapping and genome sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence mapping by electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones that contain the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well." In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clone's, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

<u>Seq. ID No.</u>	<u>Identified BACs</u>			
4	195/N/3	206/P/3	384/I/3	323/G/9
5	222/B/10	404/E/10	526/F/20	565/P/11 279/F/14
9	501/L/21			
11	490/P/4	321/I/23	410/F/5	443/N/20
19	311/A/19	505/F/17	216/D/8	219/C/22
29	382/N/10	539/L/7		
31	530/D/11			
35	503/N/10			
37	547/D/16	215/P/16	439/K/6	
39	216/L/9	512/F/5	203/J/15	
45	205/K/7	250/H/22	283/C/17	528/B/20 402/L/11
80	371/A/20	470/L/3	495/L/3	
92	254/M/9	376/O/12	421/L/18	429/J/19
112	243/O/14	520/K/15	565/J/17	565/J/24

TABLE I**Col. 1 - Seq. ID No.****Col. 2 - Expression****Col. 3 - Function****Col. 4 - Modules****Col. 5 - Cytogenetic localization****Col. 6 - Nearest marker**

TABLE I

Seq. ID No.	Expression	Function
1	Overexpressed in ovarian tumor tissue	Unknown
2	Overexpressed in ovarian tumor tissue	Unknown
3	Overexpressed in ovarian tumor tissue	Unknown
4	Overexpressed in ovarian tumor tissue	P52r1PK
5	Overexpressed in ovarian tumor tissue	Unknown
6	Overexpressed in ovarian tumor tissue	Unknown
7	Overexpressed in ovarian tumor tissue	Unknown
8	Overexpressed in ovarian tumor tissue	Unknown
9	Overexpressed in ovarian tumor tissue	Unknown
10	Overexpressed in ovarian tumor tissue	Unknown
12	Overexpressed in ovarian tumor tissue	Unknown
13	Overexpressed in ovarian tumor tissue	Unknown
15	Overexpressed in ovarian tumor tissue	Unknown
16	Overexpressed in ovarian tumor tissue	Unknown
18	Overexpressed in ovarian tumor tissue	Unknown
19	Overexpressed in ovarian tumor tissue	Unknown

TABELLE I

Seq ID No.	Expression	Funktion	Module	Cylogenetische Lokalisation	nearest marker
1	in Ovariumorgewebe überexprimiert	unbekannt		1p31.1-p34.1	SHGC-2542; 2540; 2456; D1S448- D1S500;; WI-6555; D1S198-D1S462
2	in Ovariumorgewebe überexprimiert	unbekannt		2p22.3-p23.3	SGC32173; D2S174; D2S390;; TIGR- A006H24; D2S392-D2S390
3	in Ovariumorgewebe überexprimiert	unbekannt		4p15.1	WI-15951 (D4S1043; SHGC-16179)
4	in Ovariumorgewebe überexprimiert	P52rlPK		11q13.5 - q14.1	SHGC-31396 (SHGC-32287, D11S4681)
5	in Ovariumorgewebe überexprimiert	unbekannt		1q22	SHGC-31641
6	in Ovariumorgewebe überexprimiert	unbekannt		13q33.1 - q34	AFM310yd5
7	in Ovariumorgewebe überexprimiert	unbekannt		8q11.23-q12.1	SHGC-32002; D8S1828-D8SS507
8	in Ovariumorgewebe überexprimiert	unbekannt		4q24	SHGC-36699
9	in Ovariumorgewebe überexprimiert	unbekannt	PRO_RICH	2q35	SHGH-32531 (D2S1297, SHGC-35278)
10	in Ovariumorgewebe überexprimiert	unbekannt	PHD		
11	in Ovariumorgewebe überexprimiert	unbekannt		5q23.3-q31.1	AFM200ya9=D5S414
12	in Ovariumorgewebe überexprimiert	unbekannt		3p23	WI-6841; D3S1599-D3S1583
13	in Ovariumorgewebe überexprimiert	unbekannt		6q22.1-q24.3	SHGC-33316; D6S453-D6S311
14	in Ovariumorgewebe überexprimiert	unbekannt	NLS_BP	10p15.3	CDa1hh03; D10S533-D10S594;; SHGC- 11812; D10S558-D10S591
15	in Ovariumorgewebe überexprimiert	unbekannt			Cda17g12; D15S209-D15S198
16	in Ovariumorgewebe überexprimiert	unbekannt		15q21.3-q22.1	Ribosomal_L24e
17	in Ovariumorgewebe überexprimiert	unbekannt		11q14.3	SHGC-36010 (D11S1979, D11S1887)
18	in Ovariumorgewebe überexprimiert	unbekannt			
19	in Ovariumorgewebe überexprimiert	unbekannt			

Seq. ID No.	Expression	Function
20	Overexpressed in ovarian tumor tissue	Unknown
21	Overexpressed in ovarian tumor tissue	Unknown
22	Overexpressed in ovarian tumor tissue	Unknown
23	Overexpressed in ovarian tumor tissue	Unknown
24	Overexpressed in ovarian tumor tissue	Unknown
25	Overexpressed in ovarian tumor tissue	Branchio-oto-renal syndrome candidate gene
26	Overexpressed in ovarian tumor tissue	Unknown
27	Overexpressed in ovarian tumor tissue	Unknown
28	Overexpressed in ovarian tumor tissue	Unknown
29	Overexpressed in ovarian tumor tissue	Unknown
30	Overexpressed in ovarian tumor tissue	Unknown
31	Overexpressed in ovarian tumor tissue	Unknown
32	Overexpressed in ovarian tumor tissue	Partially homologous to <i>R. norvegicus</i> calpain
33	Overexpressed in ovarian tumor tissue	Partially homologous to human mRNA for fungal sterol-C5-desaturase homolog
34	Overexpressed in ovarian tumor tissue	Partially homologous to human GPx-3 mRNA for plasma glutathione peroxidase
35	Overexpressed in ovarian tumor tissue	Partially homologous to homo sapiens CHD2 mRNA

Seq ID / Expression No.	Funktion	Module	Cylogenetische Lokalisation	nearest marker
20 in Ovariumgewebe überexprimiert	unbekannt		3q22.2-3q22.3	SHGC-34629 (SHGC-30855, SGC32794)
21 in Ovariumgewebe überexprimiert	unbekannt		3q26.33-q29	AFM308y11 (D3S2363, D3S3669)
22 in Ovariumgewebe überexprimiert	unbekannt		7q11.23	SHGC-37054
23 in Ovariumgewebe überexprimiert	unbekannt			
24 in Ovariumgewebe überexprimiert	unbekannt		4q28.1-q31.1	WI-30941;SGC30941; D4S1580-D4S427
25 in Ovariumgewebe überexprimiert	Branchio-oto-renal syndrome candidate gene		7q32.3-q33	AFMc024we9
26 in Ovariumgewebe überexprimiert	unbekannt	NLS_BP	17q23.3	SHGC-64257
27 in Ovariumgewebe überexprimiert	unbekannt		17p12-p13.2	SHGC-31370 (SHGC-35547-SHGC- 35513)
28 in Ovariumgewebe überexprimiert	unbekannt		10q22.3	Cda0wf11, TIGR-A001X23;D10S607- D10S201
29 In Ovariumgewebe überexprimiert	unbekannt		11q13.2-q13.5	WI-14303; D11S4136-D11S1314;; TIGR- A005U01; D11S913- D11S1314/RH;SHGC-14407
30 in Ovariumgewebe überexprimiert	unbekannt		7p21.3	SHGC-14339
31 in Ovariumgewebe überexprimiert	unbekannt		12p12.3	AFMb320va9
32 in Ovariumgewebe überexprimiert	Partielles Homolog zu R. norvegicus calpain		1q41	SHGC-3992 (D1S2530-D1S2568)
33 in Ovariumgewebe überexprimiert	Partiell Homolog zu Human mRNA for fungal sterol-C5-desaturase homolog	Thymosin	11q23.3	WI-19895; D11S924-D11S925
34 in Ovariumgewebe überexprimiert	Partiell homolog zu Human GPx-3 mRNA for plasma glutathione peroxidase	GSHPx	5q33.1	SHGC-10972
35 in Ovariumgewebe überexprimiert	Partiell Homolog zu Homo sapiens CHD2 mRNA		19q13.13 - q13.2	AFMb018wh1

Seq. ID No.	Expression	Function
36	Overexpressed in ovarian tumor tissue	Human homolog to <i>M. musculus</i> formin binding protein 21
38	Overexpressed in ovarian tumor tissue	Human homolog to <i>Tribolium castaneum</i> zinc finger protein
39	Overexpressed in ovarian tumor tissue	Human homolog to <i>S. cerevisiae</i> chromosome II sequence for ORF YBR1725
40	Overexpressed in ovarian tumor tissue	Human homolog to <i>Rattus norvegicus</i> rsly 1p
41	Overexpressed in ovarian tumor tissue	Human homolog to PEC-60=gastrointestinal peptide, swine
42	Overexpressed in ovarian tumor tissue	Human homolog to <i>Mus musculus</i> mCAF1 protein
43	Overexpressed in ovarian tumor tissue	Human homolog to Mouse mitochondrial genome; unidentified reading frame
44	Overexpressed in ovarian tumor tissue	Human homolog to Mouse kidney androgen-regulated protein (KAP)
45	Overexpressed in ovarian tumor tissue	Human homolog to <i>M. musculus</i> Tera
46	Overexpressed in ovarian tumor tissue	Human homolog to <i>Caenorhabditis elegans</i> cosmid T27F7
47	Overexpressed in ovarian tumor tissue	Human homolog to <i>Caenorhabditis elegans</i> cosmid T27F7
48	Overexpressed in ovarian tumor tissue	Human homolog to <i>Caenorhabditis elegans</i> cosmid K11H12
49	Overexpressed in ovarian tumor tissue	Human homolog to <i>Caenorhabditis elegans</i> cosmid C43E11

Seq ID No.	Expression in Ovariumgewebe überexprimiert	Funktion Humanes Homolog zu M. musculus formin binding protein 21	Module WW_rsp5_WWP	Cylogenetische Lokalisation 2p13.1- p16.1;RH; 2p13.1-p13.3	nearest marker sISG31094; D2S292-D2S145
36	in Ovariumgewebe überexprimiert	Humanes Homolog zu Tribolium castaneum zinc finger protein			
38	in Ovariumgewebe überexprimiert	Humanes Homolog zu S. cerevisiae chromosome II sequence for ORF YBR1725			
39	in Ovariumgewebe überexprimiert	Humanes Homolog zu Rattus norvegicus rsl1p	Sec1	17	
40	in Ovariumgewebe überexprimiert	Humanes Homolog zu PEC- 60=gastrointestinal peptide, swine			
41	in Ovariumgewebe überexprimiert	Humanes Homolog zu Mus musculus mCAF1 protein	kazal		
42	in Ovariumgewebe überexprimiert	Humanes Homolog zu Mouse mitochondrial genome; Unidentified reading frame		8p22-p23.3	BDa16f11; D8S549-D8S1733 bzw.S280
43	in Ovariumgewebe überexprimiert	Humanes Homolog zu Mouse kidney androgen-regulated protein (KAP)	oxidored_q1_N		
44	in Ovariumgewebe überexprimiert	Humanes Homolog zu Mouse Tera			1p36.31-p36.13 SHGC-11461 (D1S2565, SGC32561)
45	in Ovariumgewebe überexprimiert	Humanes Homolog zu M. musculus T27F7		12p11.21- p11.23 19q13.33-qter	SHGC-1349 (D12S1621/D12S1805)
46	in Ovariumgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid			SHGC-30173; D19S418-qTEL
47	in Ovariumgewebe überexprimiert	Caenorhabditis elegans cosmid T27F7	PRO_RICH		D2S388-D2S2181
48	in Ovariumgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid K11H12	UPF0005	10q23.1	SHGC-167+SHGC-11466; D10S551- D10S532
49	in Ovariumgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid C43E11	PRO_RICH	Xq22.3-Xq25	sISG2963; DXS1059-DXS1047

Seq. ID No.	Expression	Function
50	Overexpressed in ovarian tumor tissue	Human homolog to <i>Caenorhabditis elegans</i> cosmid C40H1
51	Overexpressed in ovarian tumor tissue	Human homolog to <i>C. elegans</i> cosmid K02D10
52	Overexpressed in ovarian tumor tissue	Human homolog to bovine inorganic pyrophosphatase
53	Overexpressed in ovarian tumor tissue	Human homolog to <i>B. laurus</i> mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex
54	Overexpressed in ovarian tumor tissue	Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein or others
55	Overexpressed in ovarian tumor tissue	Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein
56	Overexpressed in ovarian tumor tissue	Human homolog of <i>R. norvegicus</i> intestinal epithelium proliferating cell-associated mRNA sequence
57	Overexpressed in ovarian tumor tissue	Homologous to Bruton's tyrosine kinase
58	Overexpressed in ovarian tumor tissue	dbpB-like protein
59	Overexpressed in ovarian tumor tissue	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein
63	Overexpressed in ovarian tumor tissue	Protease, serine, 2 (trypsin 2)
65	Overexpressed in ovarian tumor tissue	Human annexin IV
67	Overexpressed in ovarian tumor tissue	Human X2 box repressor

Seq ID	Expression No.	Funktion	Module	Cytogenetische Lokalisation	nearest marker
50	in Ovariumgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid C40H1		1q22	WI-7155
51	in Ovariumgewebe überexprimiert	Humanes Homolog zu <i>C. elegans</i> cosmid K02D10		7p11.2-p12.3	Cda1bc08;D7S506-D7S499;; SHGC-17265+11581;D7S499-D7S2429
52	in Ovariumgewebe überexprimiert	Humanes Homolog zu Bovine inorganic pyrophosphatase	Pyrophosphatase	3q26.1	SHGC-9372
53	in Ovariumgewebe überexprimiert	Humanes Homolog zu <i>B. laurus</i> mRNA for B15 subunit of NADH:ubiquinone oxidoreductase complex		3q13.12-q13.2	D3S1310-D3S1575
54	in Ovariumgewebe überexprimiert	Humanes Homolog zu <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein aber anders		20q13.33	SHGC-11512
55	in Ovariumgewebe Überexprimiert	Humanes Homolog zu <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein	PRO_RICH; MSP_DOMAIN	15q25.3- 15q26.1	SHGC-69080 (D15S202/D15S1046, D15S1178)
56	in Ovariumgewebe überexprimiert	Humanes Homolog des R. norvegicus intestinal epithelium proliferating cell-associated mRNA sequence	PRO_RICH	1p32.2-p31.2	SGC34409
57	in Ovariumgewebe überexprimiert	Homolog zu Bruton's tyrosine kinase	rrm; PRO_RICH	10q21.1-q22.1	WI-11265; D10S581-D10S210
58	in Ovariumgewebe überexprimiert	dppB-like protein	CSD; PRO_RICH	15q25.3- 15q26.1	AFM282wg5=D15S202 (D15S1046;D15S1187)
59	in Ovariumgewebe überexprimiert	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	PRO_RICH	2p25.2-p25.1	
63	in Ovariumgewebe überexprimiert	Prolease, serine, 2 (trypsin 2)	trypsin	7q35	SHGC-16894
65	in Ovariumgewebe überexprimiert	Humanes Annexin IV	annexin	2p13.1-p16.1	SHGC-9858
67	in Ovariumgewebe überexprimiert	Human X2 box repressor		16q12.1-q22.1	WI-6174; D16S408- D16S3089;Cda01910; D16S419- D16S415

Seq. ID No.	Expression	Function
68	Overexpressed in ovarian tumor tissue	Human transcriptional coactivator PC4
69	Overexpressed in ovarian tumor tissue	Human tetratricopeptide repeat protein
70	Overexpressed in ovarian tumor tissue	Human tax1-binding protein TXBP151
72	Overexpressed in ovarian tumor tissue	Human prothymosin alpha
73	Overexpressed in ovarian tumor tissue	Human profilin
74	Overexpressed in ovarian tumor tissue	Human pepsinogen C
76	Overexpressed in ovarian tumor tissue	Human osteopontin
78	Overexpressed in ovarian tumor tissue	Human non-histone chromosomal protein
79	Overexpressed in ovarian tumor tissue	Human mRNA for protein disulfide isomerase-related protein P5
80	Overexpressed in ovarian tumor tissue	Human mRNA for KIAA0332
81	Overexpressed in ovarian tumor tissue	Human mRNA for KIAA0078
82	Overexpressed in ovarian tumor tissue	Human mRNA for 90-kDa heat-shock protein
83	Overexpressed in ovarian tumor tissue	Human major nuclear matrix protein
84	Overexpressed in ovarian tumor tissue	Human Ku (p70/p80) subunit
85	Overexpressed in ovarian tumor tissue	Human interferon-induced 17-kDa/15-kDa protein
86	Overexpressed in ovarian tumor tissue	Human hsc70 gene for 71 kd heat shock cognate protein
88	Overexpressed in ovarian tumor tissue	Human gamma-interferon-inducible protein (IP-30)

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
68	in Ovariumgewebe überexprimiert	Human transcriptional coactivator PC4		5p15.1	SGC32812; D5S477-D5S651
69	in Ovariumgewebe überexprimiert	Human tetraricopeptide repeat protein		5q33.2-q33.3	TIGR-A002Q13; D5S412-D5S422
70	in Ovariumgewebe überexprimiert	Human taxi-binding protein 1XB1P151		7p14.1-p21.3	SGC31789; D7S516-D7S632
72	in Ovariumgewebe überexprimiert	Human prolymosin alpha			
73	in Ovariumgewebe überexprimiert	Human profilin	profilin	17p13.3	
74	in Ovariumgewebe überexprimiert	Human pepsinogen C	asp	6p21.1	SGC35331; D6S426-D6S271
76	in Ovariumgewebe überexprimiert	Human osteopontin	Osteopontin	4q13.3-q22.1	SHGC-9669; D4S1542-D4S1544
78	in Ovariumgewebe überexprimiert	Human non-histone chromosomal protein	HMG14_17	21q22.3	
79	in Ovariumgewebe überexprimiert	Human mRNA for protein disulfide isomerase-related protein P5	thioredd	2p23.3-p24.1	SGC31703; D2S287-D2S131; siSG1958; D2S162-D2S287
80	in Ovariumgewebe überexprimiert	Human mRNA for KIAA0332		3p21.1	SHGC-14798 (D3S4210, SHGC-11985)
81	in Ovariumgewebe überexprimiert	Human mRNA for KIAA0078	PRO_RICH		SHGC-9647; D7S651-D7S477; Wi- 14191,D8S269-D8S1799 +2 weitere auf Chr.8
82	in Ovariumgewebe überexprimiert	Human mRNA for 90-kDa heat- shock protein	HSP90	4, 11, 1, 6	SHGC-11305
83	in Ovariumgewebe überexprimiert	Human major nuclear matrix protein	RBD; ZF_MATRIN	5q31.1	SHGC-3183
84	in Ovariumgewebe überexprimiert	Human Ku (p70/p80) subunit		2q34-q35	SHGC-11966; D2S2382-D2S164;; Wi- 8140,D2S143-D2S164
85	in Ovariumgewebe überexprimiert	Human interferon-induced 17- kDa/15-kDa protein	ubiquitin	1p36.31-p36.32	
86	in Ovariumgewebe überexprimiert	Human hsc70 gene for 71 kd heat shock cognate protein	HSP70	11q23.3-q25	D20S113-D20S97
88	in Ovariumgewebe überexprimiert	Human gamma-interferon-inducible protein (IP-30)		19p13.13	SHGC-32638; D19S899-D19S407

Seq. ID No.	Expression	Function
89	Overexpressed in ovarian tumor tissue	Human fatty acid binding protein homolog (PA-FABP)
90	Overexpressed in ovarian tumor tissue	Human enhancer of rudimentary homolog
91	Overexpressed in ovarian tumor tissue	Human deleted in split hand/split foot 1 (DSS1)
92	Overexpressed in ovarian tumor tissue	Human decay-accelerating factor mRNA
93	Overexpressed in ovarian tumor tissue	Human chromosome segregation gene homolog CAS
94	Overexpressed in ovarian tumor tissue	Human carcinoma-associated antigen GA733-2, human epithelial glycoprotein (EGP)
95	Overexpressed in ovarian tumor tissue	Human calmodulin
96	Overexpressed in ovarian tumor tissue	Human Bax alpha
97	Overexpressed in ovarian tumor tissue	Human antileukoprotease (ALP)
98	Overexpressed in ovarian tumor tissue	Homo sapiens UDP-galactose-4-epimerase
99	Overexpressed in ovarian tumor tissue	Homo sapiens mRNA for putative progesterone binding protein
100	Overexpressed in ovarian tumor tissue	Homo sapiens mRNA for galectin-3
101	Overexpressed in ovarian tumor tissue	Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 (MIR cl-7)
102	Overexpressed in ovarian tumor tissue	Homo sapiens Kunitz-type protease inhibitor
103	Overexpressed in ovarian tumor tissue	Homo sapiens hCPE-R mRNA for CPE-receptor
105	Overexpressed in ovarian tumor tissue	Homo sapiens DNA for amyloid precursor protein
106	Overexpressed in ovarian tumor tissue	Homo sapiens CD24 signal transducer

Seq ID / Expression No.	Funktion	Module	Cylogenetische Lokalisierung	nearest marker
89 in Ovariumgewebe überexprimiert	Human fatty acid binding protein homologue (PA-FABP)		17p11.2	SHGC-9883
90 in Ovariumgewebe überexprimiert	Human enhancer of rudimentary homolog	ER	14q22.3-q24.2	WI-8921; D14S63-D14S251
91 in Ovariumgewebe überexprimiert	Human deleted in split hand/split foot 1 (DSS1)		7q21.3-q22.1	D5S1977-D5S428 (Hs.85215)
92 in Ovariumgewebe überexprimiert	Human decay-accelerating factor mRNA		1q32.2	SHGC-11228
93 in Ovariumgewebe überexprimiert	Human chromosome segregation gene homolog CAS	IBN_NT	20q13	
94 in Ovariumgewebe überexprimiert	Human carcinoma-associated antigen GA733-2, Human epithelial glycoprotein (EGP)	Igryoglobulin_1	2p15-p21	AA1113218; D2S119-D2S337
95 in Ovariumgewebe überexprimiert	Human calmodulin	EF_HAND_2	2p16.3-p21	WI-9106; D2S391-D2S123
96 in Ovariumgewebe überexprimiert	Human Bax alpha	Bcl-2	19q13.3-q13.4	
97 in Ovariumgewebe überexprimiert	Human antileukoprotease (ALP)	wap	20q13.13-q13.2	WI-6969 (D20S880, SGC34003)
98 in Ovariumgewebe überexprimiert	Homo sapiens UDP-galactose-4-epimerase	3Beta_HSD	1p36.11	SHGC-11459 (RH420-D1S3295)
99 in Ovariumgewebe überexprimiert	Homo sapiens mRNA for putative progesterone binding protein		4q31.1	SHGC4-275
100 in Ovariumgewebe überexprimiert	Homo sapiens mRNA for galectin-3	Gal-bind_lectin	14q12-q22.3	D14S276-D14S66
101 in Ovariumgewebe überexprimiert	Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 (MIR cl-7)	7Im_1; G_PROTEIN_RECEP OR_2; PRO_RICH	12q14.2-q14.3	SHGC-33073
102 in Ovariumgewebe überexprimiert	Homo sapiens Kunitz-type protease inhibitor	Kunitz_BPTI;	19q13.2	TIGR-A007F08; D19S421-D19S408
103 in Ovariumgewebe überexprimiert	Homo sapiens hCPE-R mRNA for CPE-receptor	PRO_RICH	7q11.23	
105 in Ovariumgewebe überexprimiert	Homo sapiens DNA for amyloid precursor protein	Kunitz_BPT	21q21.2-q22.11	WI-8962; D21S265-D21S260
106 in Ovariumgewebe überexprimiert	Homo sapiens CD24 signal transducer		6p21	AFM115xh2; SHGC-13799 - SHGC-32498

Seq. ID No.	Expression	Function
107	Overexpressed in ovarian tumor tissue	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16)
108	Overexpressed in ovarian tumor tissue	Histone H2B
110	Overexpressed in ovarian tumor tissue	H. sapiens, gene for membrane cofactor protein
111	Overexpressed in ovarian tumor tissue	H. sapiens TROP-2 gene
112	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for Icin protein
113	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for BiP protein
114	Overexpressed in ovarian tumor tissue	H. sapiens HE4 mRNA for extracellular proteinase inhibitor homolog
115	Overexpressed in ovarian tumor tissue	H. sapiens for neutrophil gelatinase associated lipocalin
116	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for Sm protein G
117	Overexpressed in ovarian tumor tissue	H. sapiens for glutathione peroxidase-GI
120	Overexpressed in ovarian tumor tissue	CDC28 protein kinase 2
121	Overexpressed in ovarian tumor tissue	B-factor, properdin
122	Overexpressed in ovarian tumor tissue	Annexin II
123	Overexpressed in ovarian tumor tissue	ADP-ribosylation factor like 1
258	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 2
259	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 3

Seq ID No.	Expression No.	Funktion	Module	Cytogenetische Lokalisation	nearest marker
107	in Ovariumgewebe überexprimiert	Homo sapiens Atp2/3 protein complex subunit p16-Arc (ARC16)		1q31.1	SHGC-58249(D1S2602;WI-2775;WI-7265)
108	in Ovariumgewebe überexprimiert	Histone H2B	histone; Archaeal_histone	6p21.2-p21.31	WI-11733; D6S276-D6S439
110	in Ovariumgewebe überexprimiert	H.sapiens, gene for Membrane cofactor protein	sushi	1q32.1-q32.2	SHGC-12033; D1S456-D1S2891
111	in Ovariumgewebe überexprimiert	H.sapiens TROP-2 gene	Igryoglobulin_1	1p32.2-p32.3	SHGC-12661; D1S476-D1S220
112	in Ovariumgewebe überexprimiert	H.sapiens mRNA for Ichn protein		11q14.1	SHGC-31540; D11S4179-D11S937; SGC31540; D11D911-D11S1352
113	in Ovariumgewebe überexprimiert	H.sapiens mRNA for BiP protein	HSP70; PRO_RICH	9q33.3-q34.11	WI-6005; D9S282-D9S260
114	in Ovariumgewebe überexprimiert	H.sapiens HE4 mRNA for extracellular proteinase inhibitor homologue	wap	20q13.2-q13.13	SGC30446; D20S119-D20S197;WI-30446
115	in Ovariumgewebe überexprimiert	H.sapiens for neutrophil gelatinase associated lipocalin	lipocalin	9q34	
116	in Ovariumgewebe überexprimiert	H. sapiens mRNA for Sm protein G		18q21.1	SHGC-8871 (D18S484;D18S851)
117	in Ovariumgewebe überexprimiert	H. sapiens for glutathione peroxidase-GI	NLS_BP; GSHPx	14q24.1	
120	in Ovariumgewebe überexprimiert	CDC28 protein kinase 2	CKS	9q21.31-q22.1	SHGC-11195; D9S1812-D9S283; SGC31294; D9S153-D9S264
121	in Ovariumgewebe überexprimiert	B-factor, properdin	VWA_DOMAIN; TRYPSIN_CATAL; sushi; trypsin		DXS255-DXS426
122	in Ovariumgewebe überexprimiert	Annexin II	annexin	15q22.1-q22.31	WI-8600+WI-9161; D15S198-D15S159
123	in Ovariumgewebe überexprimiert	ADP-ribosylation factor like 1	arf	12q22-q23.1	SHGC-12629; D12S1727-D12S78; WI-7420; D12S346-D12S78
258	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 2			
259	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 3			

Seq. ID No.	Expression	Function
260	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 4
261	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 10
262	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 18
263	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 25
264	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 26
265	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 30
266	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 34
267	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 42
268	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 46
269	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 47
270	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 48
271	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 50
272	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 52
273	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 56

Seq ID No.	Expression	Funktion	Module	Cyogenetische Lokalisation	nearest marker
260	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 4			
261	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 10			
262	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 18			
263	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 25			
264	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 26			
265	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 30			
266	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 34			
267	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 42			
268	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 46			
269	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 47			
270	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 48			
271	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 50			
272	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 52			
273	in Ovariumgewebe überexprimiert	Verlängerung zu Seq ID No: 56			

TABLE II

Seq. ID. No.	ORF Seq. ID. No.
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Seq. ID. No.**ORF Seq. ID. No.**

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268	294	295	
269	296	297	
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271	300	301	
272	302	303	
273	304	305	

The inventive nucleic acid sequences Seq. ID Nos. 1-123 and 258-273 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 124-257 and 274-307 are described in the following sequence protocol.

Sequence Protocol**(1) GENERAL INFORMATION:****(i) APPLICANT**

- (A) NAME: metaGen - Gesellschaft für Genomforschung
mbH
(B) STREET: Ihnestrasse 63
(C) CITY: Berlin
(E) COUNTRY: Germany
(F) POSTAL CODE (ZIP): D-14195
(G) TELEPHONE: (030)-8413 1673
(H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from
Ovarian Tumor Tissue

(iii) Number of sequences: 284

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patentin release #1.0, version #1.25
(EPO)

(2) INFORMATION ON SEQ ID NO. 1:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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CTCTTCTCTC CATTAGAAA ATTAGTAAA TAATGGATTCT TATAATGGG AGCATCACCA 1200
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CATCTCAAT TTAAACATT TCTATTAGC TGATTGGTTC TCACATATAC TTCTAAAAGA 1440
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AAAACCTGTGA ACCTAACTT CTCTTATTGG TGGGTAAATAA CTGAAAATAA AGATTTATT 2040
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GTTTCTGGT TTCTGACCTG TGTGACACC CCTGTGTGTT TATAATTAA AAATTGAATT 2160
TTATATGGGG TTTTATTG CTTAAACCA GGCTGTGAA TCACATTGG GAAGGGTACT 2220
TATCTTAATG ACTAATGACT TAATTGGAA AGTGTAAATT TTGTAAAATA CAAAATCCAA 2280
GGACTCTTG GGATTTAATC TAATTGTCACT TTGTTAGGC AGATGCACCTT TTTGGATAA 2340
TGGAAAGTTA AGCATAACCGA ATGCTACTTT TGGTTGACAA ACGGGCCTAA TAGTCCGGGG 2400
----- -----

```

(2) INFORMATION ON SEQ ID NO. 2:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 798 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

gccttatattg gaagcagaca gcgatactga tgacattgac cacagagtta cagaggaaag 60
ccatgaagag ccagcattcc agaattttat gcaagaatcg atggcacaat actggaagag120
aaacaataaa taggagactt tagcacactt cacttggttc tagaagtcca gaattttggal80
cctccacgtg aaagaactgt tcttacctct gaactggggg ctcccataag ggataattt240
cctcagagta gcaaagttt tcttattaga gaaatcttgt gactcagatg aagtcaaggaa300
tagaagaccc ttggacaccttgg caggtaatg ctgattattt cttggccctt cccttgat360
tatgcaagga aggatatact gagctgatac tcttccaagc ctacaacttc aagttttatc420
atttgaactc aagtactttt gctgctgagg aatggaatca aaagaacgt a gtctcctgg480
gaccaccta gatctctattt attaggcttag atgtatagcc tctactcccc cagcttcttg540
ctcttgaccc tgcactgtaa gttgccctt tattagcagc caagaaaaag gaaaacatga600
gcttatccag aacggtggca gagtctcctt ggcaatcaac caacgttgct atgaaatatg660
cctcacactg tatagctcat tataggacgt caggtttggt gaaaaaagtg ggcaagacat720
gattaatgaa tcagaatccctt gtttcattgg tgacttggat aaagactttt taattttaaa780
aaaaaaaaaaaaaaa 798
  
```

(2) INFORMATION ON SEQ ID NO. 3:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 882 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

attccaaaca tggcggttcc actagggggt atgtttctg ggcagccacc cggccccct 60
caggccccgc cgggccttcc gggccaagct tcgccttc aggcagctcc aggcgtcct120
agacccctca gcagtacttt ggtggacgag ttggagtcat ctttcgaggc ttgcttgca180
tctctggta gtcaggacta tgtcaatggc accgatcagg aagaattcg aaccgggtt240
gatcgtgtt tccagaaggat tctggatatt gcaagacaga cagaatgttt tttcttacaa300
aaaagattgc agttatctgt ccagaaacca gagcaagttt tcaaagagga tgtgtcagaa360
ctaaggaatg aattacagcg gaaagatgca ctatccaga agcacttgac aaagctgagg420
cattggcagc aggtgttggaa ggacatcaac gtgcagcaca aaaagcccgc cgacatccct480
cagggcttcc tggccatccctt ggagcaggca tctgccaaca tccctgcacc tctgaagcca540
acgtgagcaa agggcagagg cagttggccat atgagtggc tgatgcgtga ggttgccac600
acatcccttc ctgtggactt gacatccctt aagaacttcc tggccatata tgatccatt660
ttagttttat gtccttatttgg aaaaattttc cactatccctt ataagctgtt aatcccttga720
gtactttata acatgtctgt agcttggata aaccaagtttta gtatccctt tttgttta780
gaaaatttta gactgttata atgatgacac agattccctt ttatgggtggc tttgttta840
ttaatccctt gcatgacttt taaaaaaaaaaaaaa aaaaaaaaaaa aa 882

```

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2901 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

(2) INFORMATION ON SEQ ID NO. 5:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 579 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

aaagaaaagag aaagaaaagaa aagaagattg tagcttaggg gagagtaggt gaaaagatga 60
 acaacatgac cgaaaaaggatt tcctaatctc accacagcct ggctctacct taagtcttta120
 ataaaaagttt gactgaaggtt accaagggtt gctgaagtgg aagcaaagttt ctccaaagtc180
 cagcatggta gacatcaagt gtggtaacca aggacagacc ccaaggcaag gtgaacctca240
 aaaatggAAC ctcaagtttca tgcagttccag ctgcctcccc caccagaaaag ttcttgccc300
 agcccaacat cagtgccttctt gagtttgtttt actagaaaaca aaggaaagaat ttcccttgtaa360
 aaatataagac agagtagtcc ctggctttctt cctcttgcag gaaggatggaa ttctccattt420
 ccataccatc ttccccccac actggcccca gaaataactta attcaacttat gtgaaaataa480
 agattttttt tggttgagg gcatagggtt ccatttatcc ttattttta tgaggcacta540
 aatttagctttt gtatgttattt aaatgtgtctt cgtcaatgc 579

(2) INFORMATION ON SEQ ID NO. 6:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2809 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

gcaggggcctc	gtgcccggtt	cataaataagg	tttctcaact	cttccttttt	tcctcttttt	6
atcccctca	ccctcccccta	aaccctgctt	cagcacaaatg	gactaattct	agcattctga	120
tcataaggcc	ctccattttc	ctaatgtgtt	tcaaggaatc	tttttagaa	aaatatccag	180
attattcatc	cacaaaaaaa	agtatctact	aacaactcct	tttttctct	agagagttat	240
gaaggaacag	gttgtccctg	tctggagtca	agctaaacac	atgatttgtt	ttatcagcag	300
ctggagcaga	agtgtaaaat	gtctttctgt	gagacagtaa	tttgctactg	aagctttatg	360
gcttgtttgc	actgattact	ccaggatcca	aaaacttgg	gaaagtcaact	gaaacactca	420
aggcaattt	cttacagcc	ctgagtgtct	gtcaccatag	tttgatcaat	gaatatgaat	480
cccattgggt	tgtgtatgt	gaaatccctgt	agtgttattt	tcttgaactg	aaatattttg	540
ctcaaaataa	ttaagactca	ttgtcatttt	tcatcttggc	attattgtgg	acaagtggc	600
atattaaatc	tctttcttt	ctggtaagct	tagtttttaa	aatgcatttt	cccttgcct	660
gtcttaact	agatatacat	gcttatattt	atagtgggtt	tcacagacta	aaaattgaa	720
tgtgtttttat	tttttatttt	atcagtgttt	ttataataatga	agatattttt	ggagtaatgg	780
tgctgtctt	tagcaggtt	ttaatcatag	taagattttt	ttcttcttc	ttgttttttt	840
tgtttcatat	taacaatttt	ttttttacac	ggacacaacc	ctctgacagt	cttccaaat	900
attaaaatca	tttgaatatg	tatgtgtgt	tctgaacact	gctcaagcca	tcaagcagtc	960
ttcatacagt	ttgcattata	aaatctcatt	aaattctcca	agaaaaaaaata	agttgaagaal020	
tttttatttcc	tgaccatgca	tcccctggat	ttctgagttt	cagttcagat	tgttagatgac1080	
aatataagct	gccttccgaa	attgtcaaca	tctgaatgtt	aagtccattt	ccccatggal140	
agaagcccg	agttccatga	agtatggatt	accatttgtt	tttttcaacta	acagtaatg1200	
tatttttctt	attaattgtt	tgcccttagga	atgatgaatt	acattttttt	ttcccttctt1260	
ccataaacat	ctgcattccct	cagctcagcc	ttccttggat	gttgtttttt	tataaatgg1320	
tgagctgt	atgcaggtt	tgccaaagcta	acagttacaaa	tcatttttaaa	gaggaagctg1380	
gcgcgtatgg	cagccgagga	gcacactctg	caggacactg	gacaagacag	taaattatca1440	
acttttaatg	ctgattaaag	gagtataatgt	aaagaataacg	taggtatata	taatttggta1500	
gacaaatatt	cactttattt	atattttata	tatttttttt	taatttttgtt	aaatactatc1560	
cagttttgtt	gttgtccctt	ttgattttgtt	tgatattaaa	gtatttagtaa	taattgcccag1620	
gaaactatca	ttagggaggg	tttagtttgtt	tgctgtttgg	actggggaggg	atgatttaa1680	
tttagtgtt	gaaacccaattt	tttagtactg	cacagtttat	cattttgtca	acagaaggtt1740	
gtataaaagc	taccctgtta	gtcatatcaa	aaaagttcag	aggaagat	gtaaatattt1800	
atcaataaaa	ataaacattt	ttgttttcta	atatcttaac	atatcctccc	ctttaggagg1860	
aaaaacgtgc	aaaacgttag	gagctagac	gaataacttgg	agagaataac	cgaaaaattq1920	
cagaagcaca	agccaaactg	gccgaagaa	agttgagaat	tgttgaagaa	caaagaaagal1980	
ttcatgagga	aaggatgaaa	ctagaacaag	aacgacaacg	tcaacaaaaaa	gaagaacaaa2040	
aaatttattct	ggcaagggg	aagtccaggc	aaaaactgtc	cttctcatta	aaaaaccagg2100	
attaaatgtc	aaactctgtt	ctttttacaa	agaaaaatgg	aaaaactttt	tatgttagct2160	
tcatgttgg	gtgtttttt	gtttttgtt	ttgttttttt	aattttgtt	atctggaaag2220	
ttagcttgtt	ctaatagggg	ctatgtctg	caatccccctt	ttttttttt	tttttccctt2280	
ccacttaagtc	aaatcccttat	cagatcattt	ttgtatttcta	aggagtgcac	tatttttcac2340	
ctgtttttgtt	tctatattag	ttgtctgttt	aaagagcagat	cacattgtt	aactatggat2400	
ggctctgttt	ggctttttact	gacccctact	acttcttgc	tataactctgt	ttgtctacatc2460	
ataatgttgg	ttttgttgc	ttttttgttt	tttatataatt	tataaaaaaaa	aaaaaaagtq2520	
gtgatgtcat	tggaaattt	ccagggattt	acttggaccta	tgtgggttat	tgttaaaacca2580	
gtgtcccttgc	gataactgtt	ctcttgcattt	tcctgataca	ggtaaggaaa	cagtggtca2640	
actctgtata	aaagtatata	tacagttcag	tattgtctct	gttcattttt	tttttatttc2700	
attgacaaaa	tcaaaaccagc	atccccattt	gtgtaaataa	atgattttgc	tgaataaaagt2760	
aaagtcttaa	attcaaaaaaa	aaaaaaaaaa	gaaaacaaaa	aaaaaaaaaa	2809	

(2) INFORMATION ON SEQ ID NO. 7:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 910 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

agttcggcac agagaagta tttaaccta cctgttagaga tcctcgcat gaaaaggc 60
caaactgtt tgaatgaaag gacaagtaag agtgaggcca cagttccac cacacgagg 120
ctttgtatt gttctacttt ttcaagccctt tactttctgg ctgaagcatc cccttggagt 180
gcctatgtata agttgggcta ttagagttca tggaacatag aacaaccatg aatgagtggc 240
atgatccgtg cttaatgatc aagtgttact tatctaataa tcctctagaa agaaccctgt 300
tagatcttgg tttgtgataa aaatataaaag acagaagaca tgaggaaaaaa caaaagggtt 360
gaggaaatca ggcataatgac tttatactta acatcagatc tttctataa tatcctacta 420
cttgggtttt cctagctcca taccacacac ctaaacctgt attatgaatt acatattaca 480
aagtctataaa tgtgccatat ggatatacag tacattctag ttgaaatcgt ttactctgct 540
agaattttagg tgtgagattt tttgtttccc aggtatagca ggcttatgtt tggtggcatt 600
aaattggttt cttaaaaatg ctttgggtggc acttttgtaa acagattgct tctagattgt 660
tacaaaccaa gcctaagaca catctgtgaa tacttagatt tgtagctta tcacattcta 720
gacttgtgag ttgaatgaca aagcagttga acaaaaatta tggcatttaa gaatttaaca 780
tgttttagct gtaaaaaaaaatga gaaagtgttg gttgggttttta aatctggta actccatgat 840
gaaaagaaat ttatcttata cgtgttatgt ctctaataaa gtattcattt gataaaaaaaa 900
aaaaaaaaaa 910

```

(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1447 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 671 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

agcgcgggtga agcgaaaaatggcggcggtggtagctgc tacggcgctg 60
aaggccggggggcgagaaa tgcccgctc ctccggggga ttctcgcaaggccacacagct120
aacaaggctt ctcataacag gacccgggcc ctgcaaagcc acagctcccc agagggcaag180
gaggaacctg aaccctatc cccggagctg gaatacatcc ccagaaagag gggcaagaac240
cccatgaaag ctgtggact ggcctggcc atcggcttcc cttgtggat cctccttcc300
atcctcacca agcgggaagt ggacaaggac cgtgtgaagc agatgaaggc tcggcagaac360
atgcgggtgt ccaacacggg cgagttatgg agccagaggt tcagggcttc ctcccagagt420
gccccgtccc ctgtatgtgg gtctgggtg cagacctggag gagcgtcgcc accctccttag480
gttattgtact gttaagtccct cagggttggc ccagattcca gttcgtgcct ctgaggtcca540
ccagagggcg catgaagccc aggctgtgc caaaccctac cctgccccac accaaggagc600
ccaccaaaagg caaataaaagt tattgagtgt ttagtagaaa ggaaaaaaaaaaaaaaa660
aaaagtgcac c

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671

(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 803 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

gaagatgagg aagaaga gtcAACAGCT ttGCAAAAAA CTaaaaaa ggAAATTTG 60
 aaaaATCAG agaaAGATAc aaATTCTAAA GtaAAACCCA aaggCAAAGT tcGATGGACTI20
 ggttctcgga cacgtggcag atggaaatat tccAGCAATG atGAAAGTGA aggGTCTGGC180
 aGtGAAAAT catCTGCAGC ttcAGAAAGAG gAGGAAGAGA AGGAAAGTGA AGAAAGCCATC240
 ctAGCAATG ATGATGAACC ATGCAAAAAA TGTGGCCTTC CAAACCATCC TGAGCTAATT300
 ctTCTGTGTG ACTCTTGCGA TAGTGGATAC CATACTGCCT GCCTTCGCC CTCCTCTGTG360
 ATCATCCCAG ATGGAGAAATG GTTCTGCCA CCTTGCCAAC ATAAACTGCT CTGTGAAAAA420
 ttAGAGGAAC AGTtGcAGGA TTGGATGTT GCCTTAAGA AGAAAGAGCG TGCCGAACG480
 aGAAAAGAAC GCTTGGTGTa TGTGGTATC AGTATTGAAA ACATCATTCC TCCACAAGAG540
 CCAGACTTT CTGAAGATCA AGAAGAAAAG AAAAAGATT CAAAAAAATC CAAAGCAAAC600
 ttGCTTGAAA GGAGGTCAAC AAGAACAAAG AAATGTATAA GCTACAGATT TGATGAGTT660
 GATGAAGCAA TTGATGAAGC TATTGAAGAT GACATCAAAG AAGCCGATGG AGGAGGAGTT720
 ggCCGAGGAA AAGATACTC CACCATCACA GGTcATCGTG GgAAAGACAT CTETACTATT780
 ttGATGAAA AAATAATAAC GGC 803

(2) INFORMATION ON SEQ ID NO. 12:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 828 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

agcacttcca ggctgggtg ttGTTTGGa CTGGAGAAGG GAGGCGGCGG GCGAAGGCAC 60
 gtcgagcggg ggAGCGGCGC TGCCTGTGGA GATCCGCGGA GGCCGACAGG ATTGTTGGC120
 tgccgtcccc gctgctgtgc attGGGTTAA AAACGACAAC CAACATCAGC CATGAAAGAT180
 ccaagtgcga gcaGTACTAG CCCAAGCAtC ATCAATGAAg ATGTGATTAT TAACGGTcat240
 tctcatgaag atGACAATCC ATTGCGAGAG TACATGTGGA TGGAAAATGA AGAAGAATTc300
 AACAGACAAA TAGAAGAGGA GTATGGGAA GAAGAAATTa TTGAACGCTG TTTCCAAGAA360
 ATGCTGGAAG AGGAAGAAGA GCATGAATGG TTTATTCCAG CTCGAGATCT CCCACAAACT420
 ATGGACCAAA TCCAAGACCA GTTAAATGAC CTTGTTATCA GTGATGGCTC TTCTCTGAA480
 GATCTGTGG TCAAGAGCAA TCTGAATCCA AATGCAAAGG AGTTTGTCC TGGGGTGAAG540

 tacggaaata ttGAGTGTAGA CGGGGCCCCC TTTGGTGGa TGAGCACAA TTTCCACACT600
 GTGAAGGCAG TATTAGAAGA CTTAAATTGTA AAAGCTCT TGTCACTGTG TTACACTTAT660
 GCAATTGCCAA AGTTTTGTt AGTCTTGcat GCTTAATAAA AGTGTGAGA CACTTGTAC720
 CTAAGTAAAG AGCCTGGTCC AAACCAATTt ACTGGAAAAA TAGGATTGGG GCCCCATGGC780
 CTTGGATGGT GGAAGACCAG CAAAGGGGAAG GAACCACCAAG GCCCAAGT 828

(2) INFORMATION ON SEQ ID NO. 13:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: Nucleic acid

(C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

ttgggttccg gcgccaacca atgtgggagc tgtaatagta agagcttcct aacccaaagct 60
tgttattacc gtgtgggggt tcgtttttt cgtgggtgggt tatttatttt tgattttttt120
ttcttttatg tgatctttgg gaaaacacat tcagaattat atctcgtttc tacttaaatgl80
tagtgcttag gtttaatttt ttgtactgaa gtctttattt gtgggtgcatt gctactggga240
acaagttttt gtacaaaagc ttcaatcaga atcactgtgc attactgaga ctctgtttat300
caactagcctt ctgtccctcc cgcaaaagac tggggattt aacaaaataa tatgtattt360
gatttactta aagtgtttgt aaatttctta gggacctgccc acttttgact gtggatcagt420
tgatgtacac ttgttattttt aaaggactca ataaatcact gtggctgata actgcaaaaa480
tggaaaccccg acatttgctt tgggtcctgg tgaccgctgt agccctacgt gcagtgaggc540
cttgcataat tc

```

(2) INFORMATION ON SEQ ID NO. 15:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 993 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

gcggttattaa tatttaattt atttttttt cttataaggc atgttgatgt ctatgataaa 60
 cagatgtttt gcctctgaca gcagaacttc ctttcatttt tctcattcgt tttcttttgt120
 gggtcattt ttttgaatca accacacttc attatttcia ttaagcaatt tgacaggact180
 gtttagccg cagtgtagt aaaccccttc atcgaaaact tttccatctt cccttaaaat240
 gcttgcataat gtc当地aaagggtt gtttttttttgcattt cttttggca ctagaaaatc catc当地aaaggaa300
 ccgtacaaac acgtcatcc cggctctatc ttcaatgaag acatctgact ctaaaggct360
 gggtggtatca aatttgcgtt cagagggat atacagggaa atggtaatgg tagactcact420
 aaaaggaccc gaaccaggtt ccacgtatc tgcacttggc gctgtcatct ttatccat480
 ctcttctcg ttttgcctt gaatgtatc gttcagtttc gttaagcccgttctggatggc540
 tgaatcccag tccatagact ccacggacgt gctgacccac ttggctggc catagtgtcg600
 gatctcataa cttccgggtt gggggccggc gtcctccggc gccttccagc cccggcgtctc660
 cacatgtgg gccgcccgtt cctccggccgc cccgggggtct ggctggagcg gctcggccat720
 gggccggcgtt acgtctgtgg agcctgtca gccgcccgcaga ggccccgcac cccggggccgc780
 cccggctgtcg tgcgtggcgc cccggaggtt cctccggcaga cccgggtccct840
 cctccggcc gggctggaga cccgagccca cccgatgcgt ctgcctctgg accggcgagggg900
 ggc当地ccca ccaaggccgg gccgctcac gaccccccggac agtccggcc ggagttgcgc960
 gtcctgcccc cggcccccccg cggccacagg gag 993

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ctgcaccccta	aaaaaaaaaa	aaaaaatcaa	aaaaacaaaa	aaacaaaaac	aaaaaaagaa	60
ggaaaatctt	ggagggtggg	cgtgggaact	caggaccrrca	gagtggcag	tggtgtgggg	120
agggagagcc	tctcccccc	tttctgtgt	gagaggaact	cttagtgtct	ggtcagcta	180
ttaaatgtgc	aatgtgtcaa	gtagcttgtt	ttacacgcta	caacatacgct	cattgtaaac	240
ccattgtata	agctgtgtat	ttacaaatat	aacacaacaa	ttaactttt	cottagaata	300
caaaaagtc	tgcattggct	ggggaaactat	atgctttcc	attttaagt	caggactgca	360
atactgattc	cgttaatga	gcagcttaaga	tccaatctgt	ctaatacagt	gaccccstag	420
ccatccggc	ctggcaatat	acaatttttt	ttcccccctcca	agtttgtAAC	actcccttc	480
cagaaaaggca	tttgcaaca	caggattttt	tttaaatgat	tctgaatgt	aattaacttt	540
tggagaatt	ctgtgatgcc	cttagaaagaa	attggacacg	tattgagtt	cacaaagctg	600
gggctggaa	ttgctggct	aatgtttcat	tagacttaag	aacctaataat	ttttctcagt	660
ttggtggtata	aaaccactaa	cgcttagaaa	ctgtttctc	atgcagctat	gtttcttta	720
tttatgcctt	gaggactaat	ttctggttt	ctagctgtta	atgcactgtt	gacccctata	780
atggtgccct	acgcacggca	tcccttcgt	gggggtctca	tacaggggtg	tgggcgatgc	840
atgccttatt	aagctcttg	tttcacctgg	cagtgtactg	tatcaacgta	taatacagaa	900
aaaaaaatctc	tttaaggtcc	tccttcacaa	agacatagag	tgaaactcccc	tttacatgtc	960
agtatttgtt	caacacttta	ggcaacttga	ctgtcagtgt	taaaaatgaa	aacaggaaaa1020	
tggaaaatctc	tgaccaattc	tgccacccctg	agactttcat	atagacctt	cacaacaatt1080	
gtatagatca	cacacccggct	gtatTTATA	tgtaacattt	tcacacatat	taaagatacal1140	
gaaggatataa	aaaacccccca	atgttaatgt	atttgtctaa	aaggcacaag	tttcacatat1200	
ctgtctagct	atctgttggt	aatacagaaa	gtatactact	tttttaaaaa	agtggcagal1260	
atttttgtt	atgtatatttt	gtgtgtacag	tatgtgtatg	tgttatata	tatattattt1320	
atataatagat	aatatataaa	tatTTTTT	aaggagaaaac	tagaatgttt	agctagaaaa1380	
ttcccacagcc	tgtgaagaaa	tatttcaaaa	tggccataaa	ggaggtaaaa	atgaaaaccal440	
taacctaact	tttataagagg	ctttatctt	aatttaacga	tgtgcggagg	actttcttgc1500	
ttgaatctgt	tccgggctgt	ctgctctgtc	catcaaatgg	gcaggtctgg	aatgggcac1560	
cttcggccgt	tcagaagtgg	cctgaacaga	atgctggAAC	ccaggcttga	ctcgacacal620	
ctaagggttt	gatTTGAAT	ttcagcttta	ttagaagatc	taacctaaga	gtaagctaacl680	
cacagggtatt	ctttgtaga	acactttta	tgcagatgaa	gctatTTTT	ccagcaagta1740	
gatttttcca	gttttccaa	ggagtaattt	ccccgaattt	gcataaccacg	gcgtggacag1800	
ctgatatttc	accagctgc	tggcttgggg	gtgtggctct	ttgctttata	tatatacaca1860	
cacatgtgag	tctggctggg	ctggatTTT	gtttgtatctt	cctggaaatg	agcagtgact1920	
aacgctcaca	taactgtttt	tttttttate	tgggtctgtat	aatacattt	cctaagaaaa1980	
tcatttcgtt	ttacttaaga	ggggaaagtgc	agtttttttt	tggcagtca	gaatccaagc2040	
acttgcattt	ctgggtttgg	aaaactcctt	ttttggccctt	ctatgtgttt	agccataaca2100	
attccatcaa	gcaagaaggt	aagcaaaaaga	caaaaaaaaaa	aaaggaaaa	aaaaaaaaact2160	
tgcacggct	tgtctactt	acgaaaacatg	tcggagctgt	ttgcctgggt	ggggctgggt2220	
accgtacctg	tcaatqcctg	ggatTTTCA	taaatttaqC	acqqqacata	aaq	2273

(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 986 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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gccccatata aacagtttggaa agagaaaaatg gtacagcagt tacaagagga tgtggacatg 60
gaagatgttc cttaaaaatc tctgttaacca ttcttttat gtacatttga aaatgcctt120
tggataacttgc gaactgctaa attattttat tttttacata aggtcactt aatgaaaagc180
gattaaaaga catctttccct gcattggcat ctacataatc tcagatatta cggatgttag240
attgcatctc agtgtttaaat ctttactgt agatgtactt aagtaaatca tgaaaattct300
acttgtaact atagaagtga attgtggacg taaaatggtt gtgtatattg gataatggca360
ctaggcagca ttgttatagt aactaatggc aaaaattcat ggctagtgtat gtataaaaata420
aaatattttc tgcaagtaaaa tattccctt gttaatgtta tagaaggggg gataaaaaaaaa480
ggaactaaca atttgtatgg cagtgtcaga tatttttattt ttagtatttc ctgttttgg540
ttatgtcat cttagaaagag cataatgaca ttgtttgatg aagcctaatt atgtggact600
tttttgaccc ggtttaaaccc ttctgtatagg tagttgttggta tgctggggat gagaactgaa660
taatctttgc ctggagtgtac actacactt cttttggagaa tactcagtcc720
caacttgtga ttctgtatag aacagactt acttttctag cccagcattt atctagaagc780
agaggaatcc cagcgccctt taaaagggtt tatgtggttt ttttttaaaa agctcctgtt840
tttggaaagt agaattttatg ggtacaacgt atgttcattt tttgtacata aaataaaacc900
atttaaaaag ttaaaaaaaga aaaaaaaaaag gggggaaaaaa aaaagagaaaa aaggaaagg960
aaaaaaaaaaggaggggag aagaga                                     986

```

(2) INFORMATION ON SEQ ID NO. 19:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 526 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

gcgtctatat tacatttatt gacactggat atttatttac tgtttatatac caggcaaaat 60
ggacacacca tcagtagata agacctgtat cttacgtgta agatgaaact tatgcaaag120
gcacagaaaca aattatttgt tcacagttag ttttaactct tttagcaatg cctgagtcct180
ctttatagaa acttcatttt gctaagtttag caaccattca ttttttttgt tactcttcat240
gtatagttt ctcaagtgtc tcttcaaata ctgcataatg gtatagacca tttaatattc300
caaacataat ctgaaaagact agaggaatcg ccattaattt catttgtgtt tgacaaaagcg360
tcatccaaatg gattaaaacc ttcccttttg gtggcagtgg aacggtatga tacctaaaaa420

aaaaaaaaaag ttaatcacct ctccctggata tgaatgctat tagaagtttg ttgacttctc480
ctaaatttgtat aattgccttt cttagatctat aatgtagaga gcaaaa 526

(2) INFORMATION ON SEQ ID NO. 20:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1765 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ttttttttttt tttttttttt gctgtttttt atttattttt gatttgttgc aaataataat 60
 ttattttaaa aaaatctcaa aacatgttca aacacattca gtagcaaaga tccaccattg 120
 gcacacacat taagaaaagca cacacactag gcttcttagtt gggctaatta aaatctctat 180
 gggctgaaaag gtgggttggtt gtacttaatt aagttttttt gaagtgc当地 gctatgcata 240
 acagatgagc tgaaaagctg cagagttaa gatagactt atttttcattg attttccaa 300
 agccagtcat gatatttatt taatttgtgg tcttcagggtt gcaccaatcc catqaagctc 360
 aatttgataac ttccactgt ttgtcaggta ttcatgttga aacttgc当地 tggttttgc 420
 ccgaagatcg tagagaccaa gaggtttaag aagttctgac acatctctcc agtctgc当地 480
 tcttgctacc tcagctgaag gatacttcc cagaaacttc caaagcacag gtattgccc当地 540
 tttgcctgag gtccgattga gaaatatagt agcgatgaga agtttccatg gatcatgaaa 600
 aagtgtttct tgaacgagat taaaaggta cccgaggagggtt gtc当地tttct taaaaggctt 660
 acgtcgtggg gggctaagag cttctttgtt atatttgc当地 gaaaaataaca ggcttgc当地 720
 cttttttctt atctgtgtc gtgggatggg atcttcaggta aagtcttcc tgggtggta 780
 gcaaggatggg tccatttcaag agccacgttt taaaatgtca gtatgaaat gtc当地tttcc 840
 ttccacaact tctacttttgc ttccgatttc ttcaaggatttcc aaaaaggat tccataactt 900
 ctgc当地tgc当地 tctgaggctt tggctgaaca aaatttgc当地 atgatgccag aagtttttgc 960
 ttcaagaacaa aaatttgc当地 ctgaactcaa tgatcttcc ttttttttcaaggctgtt 1020
 ttcttcactg gtc当地actgaa gggctc当地 accatgctcca gcatcagaaa tgc当地acagt 1080
 tctatcaagc tgacttttttgc tgcaacagg ttcaacttca gcatctgctt tattacacac 1140
 agatttcttctt tgcttatcac ttgaaacaaa acctgaacag ctcttccctac atccctttt 1200
 agttttcttta attgggatcc ttctcaaaaat agtc当地cttccctt cttttggct ttcttaacctt 1260
 tctgaaggatcc acatcatcaa caccctc当地 ttctttcaaa agcaaatgag tggaaagtaa 1320
 gtttagagat cctctcttccctcaactc tgaactacta cttggcggca taaacacatc 1380
 ctttttgc当地 ctgc当地tgc当地 tctgtggg tctgtgggatcc ccaaggatggaa ttgttactttt ggttttgc当地 1440
 atgggatgtc agggtgc当地 tgctgc当地 tttatatctt gacttgc当地 cccttttgc当地 1500
 aagtagacta aaatcaaaaat ttctggctt aagagaagtc tctccattt tgc当地agata 1560
 attagcaagt gaaactttgg atctgaactt cagtc当地tgc当地 gggctagaaa atgatattaa 1620
 agggaaactta ctgcttagtaa atagaaggaa cttttaaaag aactggacca catttc当地atc 1680
 ttctaaattaa ttccaaatgtt tgccatagg tatctgtcat taaaaatgaa aaaaaggatgaa 1740
 taaaatggc当地 ttttaaaatgg tttcc

1765

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 746 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

gttttttttt gttttcttta aatttggatg tctctacacc actccgttatt tgtaggacta 60
 aatacgatcta ttttttccaa tgcaaattgt gtaacattta ttttttcctt gatttttaai20
 aatacttttag tatttttaac tatgtatgtg ctttctctta cactgagttc ttttttgctc180
 ctttcagctg ctcacacaat ccttgtctgtt ggagtcatag ctgctaattc catatttattt240
 ctctacacac cttgaacatt tagtgttata ctggtaccct tctgtgttct aggaaacaaa300
 tgaattgcaa actggacttg taacaggatc atacatagag caacaaaatta gctactggct360
 ttgttaagata gtaagttagg aatttcacag tcattgtctcc aaatttcatg gcagagttta420
 aaaaacaata taagactgtg gtaaggtaca aacgaaatg caatttgcgt tgactaattt480
 ccttaggactt attttcttat gtaaaacccc tggtttttctt tccctgccac aagacagggt540
 acaaagctt ctaaaacatg ctctcaggtg tcccacacctg agacattgtt ttgtggatac600
 tctcaaaagggt gtccacaaag caaaaaaatc agaccaaattg ctaagagcaa gtaacttata660
 cctcaccacc tggacatggc actggcaaaa gtcacttcag cattagaaca gtaatgtttt720
 tgctaaattta ctaaaataat agccgc

746

(2) INFORMATION ON SEQ ID NO. 22:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 659 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

aacagactca caccagaact acattccctg gccccctgcc tggccaggcc 60
 ttgggttggca agtctgaccc gagaaaagga tctgcagaaa atcagactat ggatcactt120
 tggtttgtca ttgggaatga cattcttcc caccccgagga aaaccttgg gactttcaga180
 gacatttgtgg cttagccaacc acatggtcag cctcaaaggt gagaggctca gtaaccctcc240
 tttcccttga gaattccaaa gtgtggatgt aatttaacta gaaagccatt ggtgactatc300
 tggatccctc tggaaagtatg ctatgttgtg tataatcttgc atccaaagcc agagggaaacc360
 acaatgacta gtaaaacgggt ggtctcaatg cccacatagc ctctgcctct gaatttgcac420
 atagtggcgt tcagctgata gagcgggaag aagaaaatatg cattttttat gaaaaaaataa480
 atatccaaga gaagatggaa ctaaaatggag aaattgaaat acatctactg gaagaaaaga540
 tccaaatccct gaaaatgaaat ttgtctgaga agcaaagaca aatttggatgt acccagaaaat600
 tctgcctcggc caagaggtcc cttggatgccc accttagctgt gctccaaattt cagttttca 659

(2) INFORMATION ON SEQ ID NO. 23:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
cgcagtgcgc agccgtgggg ctctctcctt gtcatcgcc gcccgtgcg ggctgggtggc 60
tctgtggcag cgccggcgcc aggactccgg cactatgagc ggcttcagca ccgaggagcgl20
cgccgcgcggc ttctccctgg agtaccgagt ctccctcaaa aatgagaaaag gacaatatat180
atctccattt catgatattc caatttatgc agataaggta aggcatcctt gttttggac240
acagtctctt tactcagatc agcttagttct acatatgaat tttcttataat gtctctcaac300
aagtgcctaa aatgcctcggttgtgtga gtaaaggctctt gttgattagg ctggcg 357
```

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 890 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

cggaggcagc ggaaaagccga gccaggcgcc tgccgcgtgg gaagagtagg ttcaagatgc 60
 atccccggaaac ccggggcgcq ggcactgcg caggccgccc gactccgcctc agtttccgggtl20
 cggcgcaca ccaaagtccg ggaacttaag catttcggt tcttaggggt gttacaaggci80
 tgcaggagcg agatggaggt ggacgcaccc ggtgttgatg gtcgagatgg tctccgggag240
 cggcgcaggtt ttagcgaggg agggaggccag aacttcgatg tgaggccctca gtctggggca300
 aatgggcttc ccaaacaactc ctactgggtt gaccctctggc tttcatccct ttcatgtg360
 ggggtgtttc tctttgtgt tttttgccca tgacttgttc gctgatatct aaatttaagaa420
 gttggttctt gaggaaatc tgaaaatggc tacaaacttc tggataaaag aagacaggac480
 tctcaataga agaatttac acatccaagg gacccttctt tcattttac actttgttac540
 taatttgccat aacttattt attgggttagg atttcaccca ttccttagcta agttttaaa600
 attaaacccct ttgggttcgtg tttttttttt ttcaaaacatc tgatggctt acaggggctg660
 aatataaaag cattttgtact taaaggtctt gtgtattcat taagaaatat agtaatgtct720
 tttaatgtt taagagttga tcagggttta ctatgatgg caagtaatag ggatgattaa780
 taaggggaaag gtttttatgg aatttcaaaa gtcaattttat ttcaaaagcg ggggaaaggg840
 tttttagagg aggggggccc aagggtttcc tggggtttgc cgaggaggc 890

(2) INFORMATION ON SEQ ID NO. 25:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 651 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

gccgttatattt gcataactaca tcagcaaaag gtgttgcggc tttataagcg ggcgctacgc 60
 caccccgatgt cgtgggtcggt ccagagagac aaataccgtt actttgcgtt tttgtatgaa120
 gccccggtttg aagaacataa gaatgaaaag gatatggcga aggccaccca gctgtgaag180
 gagggccgagg aagaattctg gtaccgtcag catccacagc catacatctt ccctgactct240
 cctggggggca ccccttatga gagatacgat tgcataagg tcccagaatg gtgttttagat300
 gactggccatc ttctgtgagaa ggcaatgtat cctgtattact ttgccaagag agaacagtgg360
 aaaaaaaaaa ggaggggaaag ctgggaacga gaggttaagc agctgcagga gaaacgcctc420
 cctgggtggc tttaactga agctttcccc cctgcccggaa aggaagggtga ttggccccca480
 ttgtgggtgtt atattgtgac cagaccggcgg gagcggccca tggtagaaaga gagagaccc540
 atttttcatgt ctgtcaagtg aaatatgtta cagaacatgc acttgcctca ataaaaaaatc600
 agtgaatgg taaaaaaaaa agtgcattt tagtatgcaa taataagcg c 651

(2) INFORMATION ON SEQ ID NO. 26:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1256 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

ctcgagccga attcggctcg agcttcatac tgaccatcca tatccaatgt ttcattaa 60
acattaccca gcatcattgt ttataatcag aaactctggt cttctgtct ggtggcactt 120
agagtcattt gtgccataat gcagcagtat ggagggagga ttttatggag aaatgggat 180
agtccatg accacaaaata aataaaggaa aactaagctg cattgtgggt tttgaaaagg 240
ttattatact tcttaacaat tctttttca gggactttc tagctgtatg actgttacct 300
aaactatcta aaatagagca ttttgtata tttcatctga ccattccat ccaatgttct 360
catttaaaca ttacccaga tcattgttta taatcagaaa ctctggctct tctgtctgg 420
ggcacattaga gtctttttgtc ccataatgca gcagtatggc gggaggattt tatggagaaa 480
tggggataatgtt ctcatgacc acaaataaaat aaaggaaaaac taagctgcattt tttgggtttt 540
gaaaagggtta ttatactttt taacaattct ttttttcagg gacttttcta gctgtatgac 600
tgttacttga ctttttttga aaagcattcc caaaatgttc tatttttagat agattaacat 660
taaccaacat aattttttt agatcgagtc agcataaaattt tctaaatgtc cctctatgtc 720
tggttcatct ctttcacccgt cattttatgtt ggtgtttgtc tgaagaaagg aaagaggaaa 780
gcaaaatacga attgtactat ttgtacccaa tctttggat tcattggcaa ataatttcag 840
tgtgggttat tattaaatag aaaaaaaaaa ttttggttttcc taggttgaag gtctaatgt 900
tacgttttgac ttatgtatgac cattttatgca ctttccaaatg aattttgtttt caaaataaaat 960
gaagaacccgc gttccctttt tcccttttta agtgttgcgc tggccatgc tcagagggttct 1020
ctgtggatt ccaggctggag cgggtgtata cccttctttt tcagctgttc gtgccttcct 1080
tttttttttttcc caccacaaatgt gaaacaaaata catgttctca aagatacaca gtacctactt 1140
aattccatgt gatggggagac caaaagaattt gcaagggtat ggtttggat cactgtaaat 1200
aaaaaaagggg cctggaaattt ctgtcgatcc catctctaaa aaaaaaaaaa aaaaaaa 1256

```

(2) INFORMATION ON SEQ ID NO. 27:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 694 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```
gtttctaaag gatgtgtaag aaaccaggagg taaaggctc gcgatatctt aagacatccg 60
gcgttagtacg cttcagttag ccacagcgct agagaagtag gagaagctcg cgagatctgt120
gccgttgcgg aggagactag gaggggggagg agaggggatc tcgcgaaagg aaagaggtcg180
ggagcgctcg cgagatctcg gaccacccaa cctgaaaagggt gcttaggaag ttgaaaggcc240
cagaggaggc ctccgggcaa atggccggag ctggaccgac catgctgcta cgagaagaga300
atggctgttg cagtcggcgt cagagcagct ccagtgctgg ggattcggac ggagagcgcg360
aggactcggc ggctgagcgc gccccgacgc agctagaggc gctgctcaac aagactatgc420
gcattcgcac gacagatgga cggacactgg tcggctgttt cctctgcact gaccgtgact480
gcaatgtcat cctgggctcg ggcgaggagt tcctcaagcc gtcggattcc ttctctgccc540
gggagccccc tggtctggc ctggccatgg taccggaca ccacatcggtt tccattgagg600
tgcagagggg gactctgacc gggcctccgt atctctgacc acgatggcgc ttacctttca660
gacttcatta aacttatgac cgaaaaaaaaaaaa 694
```

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1927 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

gcgagttttt atttttttt tttttttt acagaaattt acctttttt gttgtactaa 60
aggctgtta acttttgata caaagtaaca ttttagtaca gaaaatccca gtctgtcagc 120
ttagtacctg tctgtcaca ctgtaccatc tcagtcaccc tctgcctgtt acttagaaaa 180
caaaaaatccac cccccagaggg tctgcagtt aataacctga gaatagtcta cagttttca 240
tagtttgtct gagctagaaa acttgtaccc taaaacacaaa ggacagcatt gaggactgaa 300
acttgtctct tttttgaaca actgtgcaag aaaatatacc cttttttaaa aaacatcatgt 360
tatggctaaa ctacaatcta gtgtcttagaa ttacaaagaa taaaatgaaa tcaaagattt 420
ctcgcttagta aatgaaatg ttaggaacag tattaaaata taggtcctac cccaacgaca 480
cttacacaga gcccagtaca gtacccat ttaacaggac gcatacgctt aggaggaacc 540
acatcaaattc ttcaggcaga catatcttc ctcagaatgt caaaaaaaaaaaa aaaagcccc 600
aaacgaagac accccacactg agttaggggtgc atgcccgtgat tgctgtatc aagattaaaa 660
agacctcagt tttttttt agactgttga tagtgcata aaccattatg ctccccctaa 720
aagctctcaa ttcaatgtct gaaacatgaa tgtttccata tcaaaaaagaa ctgatgtacc 780
tgccaccctc taaaaagttt aagaattacc ctgcaaacat tgcactgtatc aaggctgtca 840
cgacttacag agcctaagga ggacccaatg gcaggcatca gcacagctga acaccaccc 900
gacccactg cagccctgcc cacgcagctc tcacggagca gacacagtcc tcaagtaata 960
agcacatgtt gaggagaaac gagaggctgt ggaaggcagg agagaaaggc cgagagacgal020
ttttgtttaa atgccaaagt cacccccc attgtgggag gaaaatgcca aaggcactgg1080
ttctgtgtcc acaggcagtc tgagcacctg gagttgtgac gtccttccag gagaggtgcc1140
accaaggagc aggaggtttt tcaaagctct ggtccacca acaagaacct cccaaagcaal200
agcagccccc attgaggttc caaggtcgtt ttgttgcata cggaaacgaa accaacacca1260
aagcgacagg ggggttgcac aggggacagg ggctggcac cggcaacatg gagccgttca1320
agtaaacata aaccacccaa tacttagaaa aggctgtaa accagtgtatc cgaaagggtc1380
tctttgcagc atctctgtatc agctggctaa agaaagggtgg gtgtgttgc accgttttagt1440
gttatctgtt ttgtgttaaa gcacacgtgt gacacgggca gagttgtgtgg gcttggccct1500
ggatcgacag cagccgtggc cctctgtcta caaaggaggt gcttctgggt cctgggtccg1560
gatccccc cccatgttc atagacggac agacttctac tttcagtcgc tagaaaagag1620
ctgagtctgg tttccctca ggcggccagc tgcagtcata cacagcacag cattctccct1680
gagcggccag gctggaatcc acaggacttt attttgcata tgattgacca ttgccaagat1740
ctgagtgc当地 atgctgtaca gggctccctc ctggatgacc cctgcaaaag agccccccag1800
acacgtcatt cagctcagag taagacccca gtttgaggc aaggcagttc agctgtcact1860
ctttctactg tttggctgtc tgctttgtgc tccttggcac tctgtccat ccccacctga1920
ctctccct 1927

(2) INFORMATION ON SEQ ID NO. 29:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 672 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vi) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

gccttttat tttttttttt tggtcgttat gctgcattta ttatgagaat caacagtcaa 60
cagttaatga ttgactaact ctttgtgttc actctggaca ttaacgaaaa agactggaat120
agggctacag cgctgttttt atgctacacg ggttatgctt ggactctgac tcccgacgc180
aggtagattc aggaattcat ggcagtgaca ttcaccatca tgggaaacac cttccctttt240
cttcaggatt ctctgttagtg gaagagagca cccagtgttg ggctgaaaac atctgaaagt300
agggagaaga acctaaaata atcagtatct cagagggctc taaggtgcca agaagtctca360
ctggacattt aagtgcacaa aaaggcatac tttcggaaatc gccaagtcaa aactttctaa420
cttctgtctc tctcagagac aagtgagact caagagtcta ctgttttagt ggcaactaca480
gaaaactggt gttaccccaga aaaacaggag caatragaaa tggttccaaat atttcaaagc540
tccgcaaaca ggtatgtgtt ccctttgccc atttagggtt ttttctcttt ctttctctt600
tgttttagttc tcgttctttt tttcagtttc catcagatct cccccctcgatccactggaaat660
ctcagagggtt gc 672

(2) INFORMATION ON SEQ ID NO. 30:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 269 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

ccgcatecta gcccggact cacacaaggc aggtgggtga ggaaatccag agttgccatg 60
gagaaaaatc cagtgtcgc attcttgcgc cttgtggcgc ttccttacaa tctggccagg 120
gatagcacag tcaaacctgg agccaaaaag gacagaagg agtctcgagc caaactgcgc 180
cagaccctct ccagaagttg gggtaacaa ctcatctgga ctcagacgta tgaagaagct 240
ctatataaat cgagacttgc aactaacc 269

```

(2) INFORMATION ON SEQ ID NO. 31:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 604 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

tgcgaggcg ggatagttgt ccaaggctc cccagcact gaggagctcg cctgctgcc 60
tcttgcgcgc gggaaagcagc accaagtca cggccaacgc cttggcacta gggccagaal 20
tggctacaac agtccctgat ggttgcgcga atggcctgaa atccaaatgc tacagacttt 180
gtgataaggc tgaagcttgg ggcatcgcc tagaaaacggt ggcacagcc ggggttgtga 240
cctcggtgc cttcatgctc actctcccgta tcctcgctcg caaggtgcag gactccaaca 300
ggcggaaaaat gctgcctact cagtttctct tcctcctggg tttgttggc atctttggcc 360
tcaccttcgc cttcatcatc ggactggacg ggagcacagg gcccacacgc ttcttcctct 420
ttgggatct cttttccatc tgcttctct gcctgctggc tcatgtgtc agtctgacca 480
agctcgcccg ggggaggaag cccctttccc gggttgggtat tctgggtctg gccgtggct 540
tcagcctagt ccaggatgtt atcgctattt aatatattgt cctgacgatg aataggacca 600
aggt 604

```

(2) INFORMATION ON SEQ ID NO. 32:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 781 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

ctttaatgtg cctagagcaa tggaaatgggg cactttgggg gcggtggaat tcaagacgct 60
ctggctgaag attcagaagt atctggtaac tcctctttcc ttctggcat cctcttcctct 120
gttctaattcc tcccttacac tcatttctgg tccattgtat tctgaccaca tccttaatca 180
tggtcaaaac tattgagtc tgggcacatt ggtcatgaag gaacaagaag gcaatgagag 240
actctcatgc caaccactgc cctgaaagcc ctgctgttca gacagcaaaag gggccagcac 300
tggccaagct ctatgttgc ctctgaaaacc ttcttgggag gagtcaatacg ggtctccctt 360
tgaaagtgtc cctggcctt tgagaaagca gtgtggtggg gggagatggt tctggcagg 420
gccgtgaatg gtgttttct acttgggatt tctttccctgc ttttaggagat ctattggaa 480
actgattata accactcggt caccatcgat gcccacgaga tgaggacagc cctcaggaa 540
gcagggttca ccctcaacag ccaggtgcag cagaccattt ccctgcggta tgcgtgcagc 600
aagcttggca tcaactttga cagttctgt gcttgtatga tccgccttggg gaccctctt 660
aaactattca gccttcttggg cgaagacaag gatggcatgg ttcagcttc tctggccgag 720
tggctgttgtc gctgttgttggt ctgaccggcc aaacttgacc tagaagatgg ggggggcctc 780
c

```

781

(2) INFORMATION ON SEQ ID NO. 33:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
ggccactgcs gcgagacgcg aggaactgtc gctcgactc gtgcgcctcg ctttgctttt 60
cctccgcaac catgtctgac aaacccgata tggctgagat cgagaaattc gataagtgcgal20
aactgaagaa gacagagacg caagagaaaa atccactgcc ttccaaagaa acgattgaac160
aggagaagca agcaggcggaa tcgtaaggag gcgtgcgccc ccaagtatgc actgagatgc240
gagaagtgtt gcgtcgaatt tacctgcttg agggggtaaa gttgggaagg tggaaaaggg300
gtgg 304
```

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1528 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
aattcggatc catgggccac agtggatggc ttgaaaatgtg gctgagcgct tcggacactt 60
cgatccatg gtggccaccc caagacgcgc cccagccgc catggcccg atcctccggg 120
atcctgcctt ctgtccctgc tcctggccgg gtttggccgg ccggggccggg gacaagagaa 180
gtctaagaca gactgccatg gcggtatgag tggtaccatc tacgagtatg gagccctcac 240
catcgatggg gagaataca ttccctttaa gcagtatgca ggcaaataata tcctctttgt 300
caacgtagcc agctactgag gtctgacaga ccaataacctt gaactgaatg cactacaaga 360
agaacttggg ccattttggct tggtcattct gggcttccct tccaaccaat ttggcaaaca 420
ggagccaggc gagaactcgg agatactccc cagtcgcaag tatgttcgac caggtggggg 480
ctttgtgcct aatttccagc tctttgagaa aggagatgtg aacggggaga aagagcagaa 540
attctacact ttcttgcaga actctctgccc tcccactgca gaactccctgg gctcacctgg 600
ccgcctctt tggaaaccca tgaagatcca tgacatccgc tggacttgc tggacttgc 660
ggtggggcca gatggcatac cggttatgct ctggtaccac cggaccacag tcagcaacgt 720
caagatggac atctctgtctt acatgaggcg gcaggcagcc ctgagcggca gggggaaagta 780
actgatgccc ccacccctacc cctacccctt gcccacatg caagggccga ggaggggctc 840
ttcaggaagg aagccccatt cccagtcatt ctaccccccac cccagatct ctttttatt 900
acataaaaaga caagccctggc acaactgtgt gtctgaacca ctgtggacac gtgacaattg 960
```

tcccagtgtg tgcatggctt cacagccacq tatctgcctg cttgaaacccc aaggatggtc 1020
 catctgtttt tacggcttgg cacaacaccc tcataaaaaa tttagctttt gttccaaat 1080
 gagcccaaag gaaacacaag ttctaggtcc aatggttctg ctcaaacctg aacatcatt 1140
 ttggggccag catatccccac atgcccacac tacacacccac cagcccttc 1200
 gaaggaccct cctgagcccc caagccatc ccacagtgtc cctgagacca gccaaagaca 1260
 ctgtgagccgc gatggcccg 1320
 cggccatc gtgggcgggc 1380
 cggccatc gtgggcgggc 1440
 cggccatc gtgggcgggc 1500
 tcactctgtc cactggatc tcaacacccc catctgccc gtaaaggctt ttctgca 1528
 aaaaaaaaaa agaaaaaaaaaaaaaaaaa

(2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ggcagggtctc agcgcttc cccctgttcc gtcctctgc agggcccaagg cgcccttggc 60
 ctttaggaccc aacttctttt accggccatgg agttcgacct gggagcagcc ctggagcc 120
 cctcccaagaa gcccgggtg gggggccggc acgggggaga tcccaagctc agtccccaca 180
 aagttcaggc cccgtcggag gcaggggcaag gtccgggtcc aaagcaaggaa caccacagct 240
 cttccgactc cagcagcagc tccagcgatt cggacacggg tttgaagtcc caccgtgt 300
 gctccaagca gcacgagagc atccgggca aggccaagaa gcccaaagtg aagaagaagg 360
 agaaggggcaa gaaggagaag ggcaagaaga aggaggtcc ccactgaagg gcccctggaca 420
 gggctcatta aaccttc tctgcctacg agtacccaacc acctggagct aagatgctta 480
 ggtgggggggg gggccggca 499

(2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1396 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gggcacccgt tagttggaa cagcggAACG ctggccccgg ggactgagta aggtgtctgg 60
atcgaggaga ggttcgggtg ggcattgggc ggctggaaaga gctcgactcg tcccgtggg 120
aaagcgcgag tctgagtggc accctggacg acttgcagag cgctggcgc agtcatggcg 180
gactactgaa agtcacagcc aaagaaaattc tgtgattact gcaagtgcgt gatagcagac 240
aataggccta gtgttgaatt tcatgaaaga gaaaaaaatc ataaggaaaaa tgtggcaaaa 300
aggatcagtg agattaaaca gaaaagcctg gataaggcaa aggaagaaga aaaggcatca 360
aaggagtttgc ctgcaatggc ggcagctgcc ctgaaaagcat accaagagga tttgaaaaga 420
cttggcttag agtcagaaat tttggagcca agcataaacac cagtaaccag cactatccca 480
cctacctcga catcaaatca acagaaagaa aagaaaagaga agaagaaaaa aagatccctc 540
aaaggcaga tgggtagaag gcataaacctc tgagggttac cattactatt atgatcttat 600
ctcaggagca tctcatgtggg agaaaacctgaa aggattcaa ggagacttaa aaaagacagc 660
agtgaagacc gtttgggttag aagggttaag tgaagatggg ttaccttactataataac 720
agaaaacagga gaatccagat gggagaaacc tgatgatttc atccacacaca ctatgtatct 780
gccttcttagt aaggtaatg aaaaattcact tggcaccccta gatgaatcca aatcatcaga 840
ttcgcatagt gattctgatg gggAACAGGA agcagaagaa ggaggggtct ctacagagac 900
agaaaagccaa aaaataaaatg ttaaggaaaaa aaataaaaat agtgatggag gaagtgaccc 960
agaaaacacag aaagaaaaaa gtattcagaa acagaattca tttaggttcaa atgaagaaaa1020
atcgaaaact cttaaagaaat caaaccata tggagaatgg caagaaaatta aacaagaggt1080
tgagtctcat gaggaggtat atttggaaact tccaaagcact gaaaatgagt atgtatcaac1140
ttcagaagct gatggggcg gagaacccaa agtggatattt aaagaaaaaa cagtcaactc1200
tcttggagtt atggcagatg gatggcccc agtcttcaaa aagagaagaa cttgaaaatgl260
ggaaaatctt agggaaaattt aaggcaacg aggtgtatgat ccaatagttt gcagggagag1320
c:tttttgcgtt acatgtttt tagggaccag aatggggaga ctttttgcca ccccccaga1380
ttgtccccgtg ttttgt 1396

```

(2) INFORMATION ON SEQ ID NO. 38:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 808 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
- (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vi) OTHER ORIGIN:
- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

cctctgtcca ctgcttcgt gaagacaaga tgaagttcac aattgtcttt gctggacttc 60
ttggagtctt tctagctcc tgccttagta actataatat caacgtcaat gatgacaaca120
acaatgcgg aagtgggcag cagtcagtga gtgtcaacaa tgaacacaat gtggccaatg180
ttgacaataa caacggatgg gactcttgga attccatctg ggattatggg aatggctttg240
ctgcaaccag actctttcaa aagaagacat gcattgtgca caaaatgaac aaggaaagtca300
tgccctccat tcaatcccc tgcactgg tcaagggaaaa gaagcttcag ggttaaggac360
caggaggacc acctcccaag ggcctgtatgt actcagtcaa cccaaacaaa gtcgatgacc420
tgagcaagtt cggaaaaaac attgcaaaaca tggcgatgg gattccaca tacatggctg480
aggagatgca agaggcaagc ctgtttttt actcagggaaac gtgctacacg accagtgtac540
tatggattgt ggacatttcc ttctgtggag acacgggtgga gaactaaaca atttttaaa600
gccactatgg atttagtcat ctgaatatgc tggcgagaaa aaatatgggc tccagtgggt660
tttaccatgt cattctgaaa ttttctcta cttagttatgt ttgatttctt taagtttcaa720
taaaatcatt tagcattgaa acggagaact ctgcgggcta gtaaccacaa ggtacggagc780
aaagatcacc caggtggaa gaggtggaa 808

```

(2) INFORMATION ON SEQ ID NO. 39:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 1139 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

ttttttttt tttttttttt ttttttcag caataacctcc tttatggat ccctgttat 60
gtccacatat gtactgtatt atcacagatg caactgattt atcatagagc actcagaaaa 120
catggaaaag tattttaaa aatcgataa tcctattcaa gtcaaccagt gttAACCCG 180
gtgtgtttcc tgccagtctg ttcccccac tgggaggtcac aaaaaatgaa aatctcctag 240
aaagagaaaat tcctctgtcc tctgacttct tcacttagta cgctgcgacc ttccccatgtt 300
gttcaacatc ctcaactcgg agcgtcaactg gctggagggtg gtttataaat ggaattggct 360
taactatctc ttcaactgaaa ggtggacatt tagggaggtgt ccagtttca gctgtcataa 420
acaactgcct tagacggcaa agaattcaca ggtcaatctgt tcccttcgct ttgaacttst 480
tcggcagaccg ttcaactgac cgaagctgga atttgctccc gtaaatgttag gaaataaaagc 540
catcggtttc cacagtgaac acgcgttta gcttggggat aacttttcagg cggctttttt 600
tggtgataat ttgaaaatg tgctttgttt cctgtagaag gattcctgtt atacccacat 660
aagagggggca ttggatttt gtcactgaaa taatagcccc gtgaagatct gccttttaaga 720
gcttggcctg aatcatctgt ggctgcgtgt ctggcttgag cccactgcac aggtccctga 780
tgcactgttt ccagagttca tgagagggaa ggaaaaggct gtatctctgc tgctctgggt 840
taatgtcaaa gagccgcagc tccttcctt gcctggcaga gaagcccttg gcttcttct 900
tcctcttcctt ggccttgtgg cgggtgaagt actccaggac caccgccttgc gctgcagct 960
ggcttcgcgc ggcctgcggg ctcatgcggg gctgtgcgc trcaggaagg ccctcacgaa1020
ggcttcggcc cgctgtgcgc ctgaaggctg gacatcgag tcattgcctt ctgtctgaga1080
caatgcattgg tagatcacac tcattcattct cggaccgctt cggcgcctt ctgatgacg 1139

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(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2177 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

acttaaaagc atratggac tagaagggga agatgaagga gccataagta tgcttctgal140
caataccgc aagctaaca cagctgttag ttcttgcca gaactcctt agaaaaaaagl200
acttatttgc ctccatacaa atgttgcac tgctgtttt aacatataa aggcaagaa1260
atggatgt tatTTGAAT atgaagaaaa aataatgac aaaactactc tggataaatcl320
tcttcttagat ataatatcg accctgtgc aggaactcca gaagataaaa tgaggttgtl380
tcttatctat tatataagca cacagcaagc accttctgag gctgatttg agcaatataal440
aaaagctta actgatgcag gatgcaacct taatccctt aatatatac aacagtggal500
ggcttttacc aagatggcct cagctccggc cagctatggc agcactacca ctaaaaccaat1560
gggtcttttca tcacgagtca tgaatacagg atcacagtt gtgatggaa gagtgaagaal620
cctggtttg aaacagcaaa atctacctgt tactcgatt ttggacaatc ttatggagat1680
qaagtcaaac cccggaaactg atgactatag atatTTGAT cccaaaatgc tgcggggcaal740
tgacagctca gttcccagaa ataaaaatcc attccaagag gccattgtt ttgtgttgggl800
aggagggaaac tacatgtaat atcgaatct tggactac ataaaggggaa aacaaggcaal860
acacatttta tatggctgc gtgagcttt taatgctaca cagttcataa aacagtgtcic1920
acaacttggc caaaagtaac acagaagaac cttactatga taatctactt ggaatgtggal980
taaatgtaaa aagaagaaaa gttagaagag caatatgttt ccttctctgt aacagtgtcc2040
taacagtgaa aatcagagtt atttgttaat tttaaggaa attatatact taatatgtat2100
tgattaaaag aaacatttca gaaataaaa ttcaacattt gaaaaaaaaa gtcggctacc2160
tacacggata atatcgc

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(2) INFORMATION ON SEQ ID NO. 41:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 402 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ggcgccaggcc ccagccagct caaggctacac tatcccagga tcagcatggc cgtccgccaag 60
tgggttaatcg cccttggcctt ggctgccctc cttgttgtgg acagggaaatg gccagtggca120
gcagggaaagc tccccttctc aagaatgccc atctgtgaac acatggtaga gtctccaacc180
tggtcccaaga tgtccaaacct ggtctgcggc actgatgggc tcacatatac gaatqaatgc240
cagctctgct tggcccccggat aaaaacccaaa caggacatcc agatcatgaa agatggccaaa300
tgctgatccc acaggagcac ctcaagccat gaagtgtcag ctggagaaca gtgggtggca360
tggagaggat atgacatgaa ataaaagatc cagcccaact ga 402

(2) INFORMATION ON SEQ ID NO. 42:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1349 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

cttcctttgc catcccattt ccttggcaact gcaccatttc cccaaattatt gcccaatccc 60
tagctttct gggtttaca atgggtgcga ccacaatca gctcatagat ggctccaatt 120
aaaaaaaaa ggtaatggtg atggataaaa taagcagatc aaggaaagtg tgctatcata 180
aaataactgt agcttcaaca tcttggatc cagttccctg gcagatagta aacatccaat 240
cacaaggat ttttcctgaa ggggttaaag ctgggttggaa aattcttcag tcacagagca 300
gcctacacat gccaattaga aactgacaga cactagatg gcttggaga ttaaacacta 360
cgtacagaaa cagcagttac taagctccctc agtagtttct tgtcttttt aagtttcgct 420
gaatcgacag ttgcacaaac gtgcataatt ctgtgggtca aaaccaagta aatactgtgt 480
aaagttggca gatTTTCCA gctaagatca agaaaaaaca aattttctga taaaacaggt 540
tttagagtca aAACACTTC taaagtgcAA aactgtatgtt ccacgatctc aaatagctaa 600
aactcctgca gaatggaaagg gagagacgtg aaacaggaa ataaattaca gtcagtgcA 660
gttaatttag gaaaaggaa aataaaacca aactcaagtc ggtaaagttt atcaaaaat 720
tcaatgtatgt agcttcccc actctctgtc acacacgctt gctaacaagt atattaaatt 780
aaggccaaat ttaacctgaa tgcgtttttt tttttctttt tattaaagatc tgagatagga 840
acgtcatac ttagtactga aaggcagaca ataaaatggg ccatgaaagg ggggggaaag 900
gtactgtcta ttgttcgagg gattcaacca gagataaaac ctatatacaa gcatgtgtgt 960
agctcgaaat aaaaataaaa ggacttatttc atgtcatgac tgcttgtgg cttcctcttc1020
atatgcattc cctgtgccat tctgtacata ggatgaacca gaaccaaggc catacaaatg1080
accacaatat ttggcatcat caatatgatc ttcaaagaac attttctctca ttttgaaaaal140
ggccattccct gtgagcaatg aatcagatcc tgcctgatgt tgtgtccctt tccgttccag1200
ctctaactgt tctgccacct cctgtaatcc acctttgaga tttttctgt catttatgat1260
gtgaagtacc tcatgaagag ctgaaaaat ctctaactgt tctgccacct cctgtaattg1320
cgagtcaatg attgacgaaa taatagtgc 1349

```

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 3552 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

attaatctt cattcttcta ctatccccaa tcctaatttc aatatcaaac ctaattaaac 60
 acatcaactt cccactgtac accaccacat caatcaaattt ctccttcattt attagccctt 120
 tacccttattt aatatttttc cacaataata tagaatatat aattacaacc tggcactgag 180
 tcaccataaaa ttcaatagaa cttaaaataaa gcttcaaaaac tgacttttc tctatccgt 240
 ttacatctgt agccctttt gtcatcatgat caattataca attctcttca tgatatac 300
 actcagaccc aaacatcaat cgattcatta aatatcttac actatccctg attaccatgc 360
 ttatccctcac ctcagccaac aacatatttc aacttttcat tggctgagaa ggggtggaa 420
 ttatatcttt cctactaattt ggatgatggt acggacgaaac agacgaaat actgcagccc 480
 tacaagcaat cctctataac cgcatcgagg acatcggtt catttttagct atagtttgat 540
 tttccctaaa cataaaactca tgagaacttc aacagattat attctccaaac aacaacgaca 600
 atctaattcc acttataagc ctattaaatcg cagctacagg aaaatcagca caatttggcc 660
 tccaccatg actaccatca gcaatagaag gcccacacc agtttcagca ctactacact 720
 caagtacaat agtagttgca ggaattttcc tactgttccg attccacccc ctcacgacta 780
 ataataactt tattttaaaca actatactt gcctcggagc cctaaccaca ttattttacag 840
 ctatttgc tctcaccctaa aacgacatca aaaaatcat tgccttcttcc acatcaagcc 900
 aactaggcc tataatagtg acgcttagaa taaaccaacc acaccttagca ttcctacaca 960
 tctgtacccca cgcatttttc aaagctatac tctttatgc ctctggctca atcattcata 1020
 gcctggcaga cgaacaagac atccggaaaaa tagaaacat cacaaaaatcc ataccattca 1080
 catcatcatg ccttagtaatc ggaaggctcg ccctcaccagg aataccatcc ctaacagggt 1140
 tctactcaaa agacctaattt atgaaagcaa ttaataacctg caacaccaac gcctgagccc 1200
 tactaattac actaatcgcc acttttataa cagctatgta cagcatacga atcatttact 1260
 tcgtaacaat aacaaaaccg cggtttccccc ccctaatttc cattaacgaa aatgacccag 1320
 acctcataaa cccaatcaaa cgccttagcat tcggaagcat ctttgcggaa tttgtcatct 1380
 catataatatttccaccacc agcattccag tcctcacaat accatgattt taaaaaacca 1440
 cagccctaat tatttcgat ttaggattcc taatcgact agaactaaac aacctaacc 1500
 taaaactatc aataaataaa gcaaattccat attcatcctt ctcaacttta ctggggttt 1560
 tcccatctat tattcaccgc attacaccca taaaatctt caacctaagc ctaaaaacat 1620
 ccctaactct cctagacttg atctggtag aaaaaaccat cccaaaatcc acctcaactc 1680
 ttcacacaaa cataaccact ttaacaacca accaaaaagg cttaaattaaa ttgtacttta 1740
 tatcattcct aattaacatc atcttaattt ttatcttata ctcaattaaat ctgcagtaat 1800
 ctcgataata ataaaaatac cgcacaaacaa agatcacccca gctactacca tcattcaagt 1860
 agcacaacta tatatgccg ctaccccaat ccctccttcc aacataactc caacatcatc 1920
 aacctcatac atcaaccaat ctcccaaacc atcaagatta attactccaa cttcatcatal 1980
 ataattaagc acacaaaatc aaaaaaccctt tataatcacc ccaactacta aaaaacc 2040
 attaatcag ttagatcccc aagtctctgg atttcctca gtagctatag cagtcgtata 2100
 tccaaacaca accaacatcc cccctaaata aattaaaaaa atattaaac ctaaaaacga 2160
 tccaccaac cctaaaacca ttaacaacca aacaaacccca ctaacaattt aacctaacc 2220
 tccataaaata ggtgaaggct ttaatgctaa cccaaagacaa ccaaccaaaa ataatgaact 2280
 taaaacaaaa atataattat tcatttatttc tacacagcat tcaactgcga ccaatgacat 2340
 gaaaaatcat cggtgtaattt caactacaga aacaccatc ggatccatga aaaacacacc 2400
 cattattttaa aattattaac cactcattca ttgacctacc tgcccccattcc aacatttcat 2460
 catgatgaaa ctttgggtcc cttcttaggag tctgcctaat agtccaaatc attacaggtc 2520
 ttttcttagc catacactac acatcagata caataacagc cttttcatca gtaacacaca 2580
 tttgtcgaga cgtaaattac gggtgactaa tccgatatac acacgcaaaac ggaggcctcaa 2640

tatTTTTTtat ttgcttattc ctcatgtcg gacgaggctt atattatggta tcataatacat2700
ttatagaaac ctgaaacatt ggagtactic tactgttcgc agtcataagcc acagcattta2760
taggctacgt cttccatga ggacaaaatat cattctgagg tgccacagt attacaaacc2820
tcstatcgc catcccataat atggaacaa ccctagtcga atgaatttga gggggcttct2880
cagttagacaa agccacccctt acccgattct tcgctttcca ctcatctta ccatttatta2940
tcgcggccctt agcaatcggtt caccctctt tcctccacga aacaggatca aacaacccaa3000
caggattaaa ctcagatgca gataaaaattt catttcaccc ctactataca atcaaagata3060
tccttaggtat octaattcata ttcttaattt tcataaccctt agtatttattt ttcccagaca3120
tactaggaga cccagacaa tacataccag ctaatccact aaacacccca ccccatatta3180
aacccgaatg atatcccta tttgcatacg ccatttacg ctcataatcccc aataaactag3240
gaggtgtccctt agccttaatc ttatctatcc taattttagc cctaataacctt ttcccttcata3300
cctcaaagca acgaagccta atatccggcc caatcacacaca aattttgtagc tgaatccctag3360
tagccaaacctt acttatctta acctgaattt ggggccaacc agtagaacac ccatttatta3420
tcatttggcca actagcctcc atctcataact tctcaatcat ctaattctt ataccaatct3480
caggaattat cgaagacaaa atactaaaat tatatccata aaaaaaaaaac acgatcggtt3540
gacatataagg gc 3552

(2) INFORMATION ON SEQ ID NO. 44:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

tttttttttttttttttt tgcaattcaa atgaacgttt atttcttaaa cccacacaga 60
gtaagggcag agcttagaga tgcctggcac agcatttctc atccaggatc acttcctcg120
tctttcttctt ttgctggag catcttagat ttatatcatt ttctacaaag acaatatcct180
gaatggcagt cgccagggtta tttcaaaagg ggagtcttctt caggaagtag gggagactgg240
attcccagct aatgaaattt tcactgtgt gtctgtgttc tcagtgaattt ctccagaaaa300
gccggaggag actgtctcaa catcgtaga gaactcagaa ttctgtttgt ttgcggctgg360
cgtgaagtcc atgatctgtt cagagtcaat gcttacaaatca tcatctgtat aatcccttag420
aggagctttt gtccctctgtt atgatcccag ttggtaaaag actgagtttta gtaggtcaat480
gattgaattt tttttttttt tatttatttta aactaattctt gacaggggaa aagccacagt540
cagaccacag aagacagtga tcaccaggac cttgaaaagc atcatgctttt agtagggttta600
a 601

(2) INFORMATION ON SEQ ID NO. 45:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2147 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

agaaggggaa caaaaaaaaaaa aatatctgaa ttttggaaaaa ccacaaaagct acaacactga 60
ccctctcttt ttttgagac ggagtttgc ttgttacc caggctggag tgcaagtggcg 120
tgatctggc tcactgcaac ttccgtctcc cggttcaag tgattctcct gcctcagcct 180
cccaagtagc tgggtttata ggtgcccggc accagaccccg gctaattttt tagtttttagt 240
agaagacgggg tttcaccacg ttggccaggc tggctttaaa tgaccctttt atttttaact 300
tggatacctg ctattctgcc aaaagacaat ttctagagta gtttgaatg ggttgatttc 360
ccccactccc acaaactctg aagccagtgt ctatgttact aaaaaaaagag ttgtatataa 420
tattnaagat gctgagttt tcatagaaa gctgaatgtct gctgtaaagt gctctttaaag 480
tctttttttt ttttaatccc cttctaatga atgaaacttag gggaaatttca ggggacagag 540
atgggatttg ttgtatgata aactgtatgt agtttttagt ctttctgttt tgagaagcag 600
tggttggggc atttttaaga tggctggcta ctcttggttt ccctcatgat aataaatttg 660
tcataactca gtaacatgaa ctggccctta gaggtatgtt ttaataattt tgaaatattta 720
aggctctgccc aagcttctgta tgattcacac ctgtactact gattattaag caggacacag 780
ttagctttct gttgcaataa ctttggagga gaaagtaatt tctaaatata cagagaggt 840
acttgactat atatgttgca tcctgtgcct cccttcatat taatatttga taaaagatttt 900
aattttatgtt aaacttctaa agcagaatca aagctccctt tggggaaatg gcaagtcttt 960
aggataggca agaccctgtt tgaatagtac caaagcattt ccgcattgtt gagaacacaci1020
tcgattttttt atgttaatgtt atctgaaaaa taaaatgtgc aagtcttcag gatggcacaal1080
aacaagggtt aatgtttttt ggggcacatt ttttagaggg ctgtctgttgcgt gtgtaaatatl1140
aatcgacttt tggttgtgtt acatgacttc tggacttca ttggaaatct gcacaatttca1200
gtttcagctc tggattactt cagttgaccc ttgtgaaggt ttttatctgt gttagaatgg1260
tggttgactt gttttagcctt attaaattttt tattttctt cactctgtat taaaagtaaa1320
acttactaaa agaaaaagagg tttgtgttca cattaaatgg ttttggtttgcgttctttt1380
gtcaggcttt ctgaacattt agatattctg aacttagagc tcttcataatcc taagatttct1440
atgaaaagcc tctcacttga acccaaaccat gagtaactt actgccttctt ttctaaatgt1500
tcaggaaaag cattgccagt tcagttttt caaaatgagg gagaaacatt tgctgcctt1560
gtaataacaa gactcagtgc ttattttttta aactgcattt taaaatttgg atagtataat1620
aacaataagg agtaagccac cttttatagg caccctgttag tttttagttt cttatctaa1680
acattttata ttcccttctt ttggaaaaaa cctacatgtt acaagccacc atatgcacag1740
actatacagt gagttgagtt ggctctccca cagtcttgc ggtgaattac aaaagtccag1800
ccattatcat cctccctgagt tattttttt gatttttttt gtacatttttgcgttcttt1860
tgggtttaga atatactata atatggatca tctctacttc tggatattttt tattttttt1920
tagacctcaa ccacagttt ctttttttttcc ttccacctctt ctttgccctgtt aggtatgtt1980
gtatgttagtc atgcactttt tatttttttta ttagaaatctt acagatctgtt tttgtacttt2040

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ttataactgtt ggataactttt aatcaaaaact tttacttaggg tattttttttt atcttagtctt2100
actaagttttt aaaaaaaaaaaa aaaaaaaaaaaa cttcaagacta gttctctt 2147

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(2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 623 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```
cccacgcgtc cccggaaacg gcggcgccgg cgacaggacc gagggggcctt agttgggtggg 60
caagtccgggg atcccagaaa gagaagcgtg acccggaagc ggaaacgggt gtccgtccca120
gctccggcct gccagtgagc ttctaccatc atggacctat tggatgttttttccggcg ccggaaagacg180
ccagaggagc tactgcggca gaaccagagg gcctgaacc gtgcattgtcg ggagctggac240
cgcgagcgcac agaaaactaga gaccaggag aaaaaatca ttgcagacat taagaagatg300
gccaaagcaag gccagatgga tgctgttcgc atcatggcaa aagacttggt ggcacccgg360
cgctatgtgc gcaagtttgtt attgtatgcgg gccaacatcc aggctgtgtc cctcaagatc420
cagacactca agtccaaacaa ctcgatggca caagccatga agggtgtcac caaggccatg480
ggcaccatga acagacagct gaagttgtccc cagatccaga agatcatgtat ggagtttgag540
cggcaggcag agatcatgga tatgaaggag gagaggattt aatttgttgcata tttgtatgatc600
ccgtgggttt tggggaaagtttt 623
```

(2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 781 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

gccccatata tgcaagcttg aaaaactaaa agatctgtga aagatgctgc caagaaggc 60
cagaaggatg tctgcatagt tctggccaag gagatgatca ggtcaaggaa ggctgtgac 120
aagctgtatg catccaaagc acacatgaac tcagtgcctca tggggatgaa gaaccagctc 180
gccccatgc gaggcttgc gaggcttgc gaggcttgc aagagcacag aagtgtatgaa gcccattgca 240
agtttgtga agattccaga gattcaggcc accatgaggg agtttgtccaa agaaatgtg 300
aaggctggaa tcatagagga gatgttagag gacactttt aaagcatgga cgatcaggaa 360
gaaatggagg aagaaggcaga aatggaaatt gacagaattc tctttaaat tacagcagg 420
gccttggca aaggccccag taaagtgact gatgccctc cagagccaga acctccagg 480
gcgtatggctg cctcagagga tgaggggggag gaggaagagg ctctggaggc catgcaggcc 540
cggtggcca cactccgcag ctaggggctg cctacccccc tgggtgtgca cacactccctc 600
tcaagagctg ccattttatg tgtctttgc actacaccc tgggtgtgagg actaccattt 660
tggagaagg tctgtttgtc tcttttattt ctctgcccag gttttggat cgcaaagg 720
tttttttat aaaagtggca taaataaatg catcattttt aggaaaaaaaaaaaaaaaaa 780
a

781

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

gttgcgacat gcagtgcgcc ggaggaactg tgctcttga ggccgacgct agggccccgg 60
 aaggaaact gcgaggcgaa ggtgaccggg gaccgagcat ttcaagatctg ctccgttagac 120
 ctggtgccacc accaccatgt tggctgcaag gctggtgtgt ctccggacac taccttctag 180
 gttttccac ccagcttca ccaaggcctc ccctgttgt aagaattcca tcacgaagaa 240

tcaatggctg ttaaacaccta gcagggaaaata tgccacccaa acaagaattg ggatccggcg 300
 tgggagaact ggc当地aaact tcaaagaggc agcattggaa ccatcgatgg aaaaaatatt 360
 taaaattgtt cagatggaa gatggttgt tgctggaggg gctgtgtt gtcggagc 420
 atgggtctac tatggcttgg gactgtctaa tgagatttgg gctatttggaa aggtgtata 480
 ttggcctcag tatgtcaagg atagaattca ttccacccat atgtacttag caggagat 540
 tggtttaaca gctttgtctg ccatagcaat cagcagaacg cctgttctca tgaacttcat 600
 gatggagggc tcttgggtga caattgggt gaccttgc gccatgggtt gagctggaaat 660
 gctggtacga tcaatccat atgaccagag cccaggccca aagcatctt gttgggtgt 720
 acatcttggt gtatgggtt cagtggttgc tccctgtaca atatttagggg gtccttctt 780
 catcagagct gcatggtaca cagctggcat tggggaggc ctctccactg tggccatgtg 840
 tgcgcccagt gaaaagtttca tgaacatggg tgcacccctt gtagtgggccc tgggtctcg 900
 ttttgtgtcc tcaattggat ctatgttttccacccatacc accgtggctg gtggccactct 960
 ttactcagtg gcaatgtacg gttggattgt tcttttcagc atgttccctc tgatgatacl020
 ccagaaagta atcaaggctg cagaagtttccatc accaatgtat ggagtccaaa aatatgatcc1080
 cattaactcg atgctgagta tctacatgg tacattaaat atatttatgc gagttgcaacl140
 tatgtggca actggaggca acagaaaagaa atgaagtgc tcaatgttgc gtttctctgc1200
 tacatccaaat atcttggat atggggcaga tatgcattaa atagttgtt caagcagctt1260
 tgggtgaagt ttagaagata agaaacatgt catcatattt aaatgttccg gtaatgtat1320
 gcttcaggc tgcctttttt tctggagaat aaatgcagta atccctctccc aaataaggcac1380
 acacattttca aatttctcatg tttgagtgat tttaaaatgt tttggtgaat gtggaaactal440
 aagtttggat catgagaatg taagtctttt ttctacttta aaatttagta ggttcaactg1500
 gtaactaaaa tttagcaaaac ctgtgtttgc atatttttt ggagtgcaga atattgtat1560
 taatgtcata agtgatttgg agctttggta aagggaccag agagaaggag tcacctgcag1620
 tcttttggat tttaaaatac ttaggaactt agcacctggg gtttatttgg ttaggtgagg1680
 gagccccgtt ggaacagccg ggtattgggg aaca

1714

(2) INFORMATION ON SEQ ID NO. 49:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 831 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
caccccccagc ccctgtctg aggcacccgag aaacgaggag gcccgtggcg agtctccacg 60
tgggtaccgg cgctctcgcc gcccgttagcc acccgccccgc cggaaagccga catctcgagt120
tctggcagaa gcaatttgcg cggcgaggag cggacgggca ggaacccaat aagctgcttc180
gcctcgggagc tgaagccgt actcaagatg gcggtcccg gcgccgtgg ccagtgacta240
gaaggcgagg cgccgcggga ccatggcggc ggcggccggac gagcggagtc cagaggacgg300
agaagacgag gaagaggagg agcagtttgt tctggtgaa ttatcaggaa ttattgattc360
agactttcttc tcaaaaatgtg aaaataaaatg caaggttttg gcattgaca ctgagaggcc420
catttgc当地 gtggacagct gtgtctttgc tggggagttt gaagacactc tagggacctg480
tgttatattt gaagaaaatg ttgaacatgc tgatacagaa gcaataata aaacagtgt540
aaaatataaa tgccatataaa tgaagaagct cagcatgaca agaactctcc tgacagagaa600
gaagggagga gaagaaaaaca taggtgggggt ggaatggctg caaataaaagg ataatgattt660
ctctatcga cccaaacatga ttgttaactt tctacatgaa aatgaagacg aagaagtgg720
agcttcagcc ccagataaaat ctttggaaat ggaagaggaa gagattcaaa tgaaccaccg780
gttcaaacccg gggtttgtt aaccggggga acccattgcg ctttggaaat t 831
```

(2) INFORMATION ON SEQ ID NO. 50:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 744 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
tgaaggttcta agagctttcc aagtttggga aggtgtccgg gttttctgcg attacttctc 60
tgagcatgaa cggaagtac ac cttttgtgcc ttatgcggtg attttaatga taggttgtcat120
atataaggacg gagtaatctg tttacatttc gttcttctcg atgcactcac aagcgggtaa180
ctaggtgaca agaaaacaaa gatcttattc aaaagaggtc ttacagcaac ccaacgtctc240
atcttcccat agtaaagatg acggcgcctt gaggttaagct acaggcaaca ccacttccgc300
gtttctctg cgccctggc caagatggcg gatgaagcca cgcgacgtgt tttgtctgag360
atccccgggtgc tgaagactaa cgccggaccc cgagatcggt agttgtgggt gcagcgactg420
aaggaggat atcagtcct tatccggat gtggagaaca acaagaatgc tgacaacgat480
tggttccgac tggagtccaa caaggaagga actcgggtgt ttggaaaatg ctggatatc540
catgacccccc taaaatatga gtttgacate gagtttgaca ttccatatcac atatctact600
actgccccca gaaattgcagt tcctgagctg gatggaaaaga cagcaaagat gtacaggtar
gactgaatag gagatggcaa agagtcaaaag aaaggccttaa ggaagaactt cgtggcgg
gggagagcat caggaagagt agct
```

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2017 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

cgcgacccga ggcgccgagc aagatggcg cgcgagtgtc ggcgcggccgc ggaggccgtg 60
 ggccggccgc ctctgcgc gggcgcccc ctgcagccctc ctgcgcaggtc tccggacatg 120
 gacatcttcc agcaacagat ctcgagaaga cagctggcta aatccttat ttgtccggaa 180
 agttgatcca agaaaagatg cccactccaa tctccttagcc aaaaaggaaaa caagcaatct 240
 atacaatatta cagtttcaca atgttaaacc ggaatgccta gaagcataca aaaaaatttg 300
 tcaagagggtt tgccaaaga ttacacgaa taaacactac ccttgtactt tggtggggac 360
 ttggAACACG tggatggcg agcaggacca agctgtccac ctctggaggt atgaaggagg 420
 ctatccagcc ctcacagaag tcatgaataa actcagagaa aataaggaat ttttggaaatt 480
 tcgttaaggca agaagtgaca tgcttcctc caggaagaat cagtcctgt tggagttcag 540
 ttcttggaaat gggctgtgc caagatccgg acctaataata tatgaactca ggttttacca 600
 actccgacca ggaaccatga ttgaatgggg caattactgg gctcgtgcac tccgcttcag 660
 acaggatggt aacgaagccg tcggaggatt ctcttcctcag attgggcagg tgcacatgg 720
 gcaccatctt tgggcttaca gggatcttca gaccaggaa gacatacggg atgcagcatg 780
 gcacaaacat ggctggggagg aattggtata ttacacagtt ccacttattc aggaaatgga 840
 atccagaatc atgatcccac tgaagacccctc gcccctccag taaagctgtt gagtttctat 900
 gtgcctacat acatttctgt gacaagtatt tgcgttaaat taattttat tgcgtatcaa 960
 gtgaaaaaga aacactgagg ttttaagctg ctgtatatacg ctgtgagaa acctctttc1020
 tttaaaattt acataatcac aaaaaaggaa agaattacag ttggactgtat tgcgtacgt1080
 ccttgcgtc ctcttggaaa caccccggtgt tgcgttgcgtt accttataac acttagccac1140
 ttctcccccac cctccagaag ggttccacgt tgaattctga atcatcttgc aaataagatt1200
 ccaaccacaa aaaaatttgc catatttct tactaaaaaa aaccaaaaaaa caaatctgtt1260
 ttataatcac agatTTTTC acaaatttct tgcgtatcgaa agaaatacaa attttgtcat1320
 gtttctcaag cagTTTTCTC gagtagtttgc tgaggaggaa caaattacaa gtttacccaa1380
 taactgaaaa tggTTTTACT cactcttattt tgcgttgcgtt accttataac acttagccac1440
 ttccaagct gggcaaggtt cattttatca gtaaatcgtt ttcacatcat gtattgtat1500
 gtttcaatgt gagacacaaaa aacaatggct tgaaactgtt gtatcatatg tgattttgaal560
 atgaacaccc tgaatagcac taattttat ttgtggattt ttcttataac aaaacaatgt1620
 gctcttagaa aagaggTTTt attttgtaaa cgttccatgg tgcgttgcgtt accttctgg1680
 ctaatatttt aataagctca cagcagatata ttcttgcgtt atgggtgagg ggttgcgtt1740
 gtttgcgtt aaattggcat aaagctgcattt tgcgttgcgtt tagctgtttt atttcatttt1800
 ttaatatagt atgccaattt tgcgttgcgtt accatgtgaa agtgcgttgcgtt aatgaacaa1860
 ttgttgcgtt cacaatcaag aatgtatgtt taaagttgttgcgtt aatggatgtt1920
 caaacttttcaatgttgcgtt aatggatgtt aatggatgtt aatggatgtt1980
 aatttccaca aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 2017

(2) INFORMATION ON SEQ ID NO. 52:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 856 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

- (vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

cgcaagtgcgc aggcgtgggg ctctctccctt gtcagtcggc gccgcgtgcg ggctgggtggc 60
tctgtggcag cggcgccggc aggactccgg cactatgagc ggcttcagca ccgaggagcg120
cgccgcgcggc ttctccctgg agtaccgagt ctccctcaaa aatgagaaaag gacaatataat180
atctccattt catgatattc caatttatgc agataaggat gtgtttcacaa tgtagttga240
agtaccacgc tggcttaatgc caaaaatggaa gattgtctaca aaggaccctt taaaccctat300
taaacaagat gtgaaaaaaag gaaaacttcg ctatgttgcg aattttttccg cgtataaaagg360
atatacttgg aactatgttg ccatccctca gacttgggaa gacccagggc acaatgataa420
acatactggc tggtgtggtg acaatgaccc aatttgcgttgc tggaaatttgc gaagcaaggta480
atgtgcaaga ggtgaaataa ttggcgtgaa agttcttaggc atattgccta tgattgacg540
agggggaaacc gactggaaag tcattgcccataatgtggat gatcctgtatc cagccaattt600
taatgatatac aatgatgtca aacggctgaa acctggctac tttagaagctt ctgtggactg660
gttttagaagg tataagggttc ctgatggaaa accagaaaaat gagtttgcgt ttaatgcaga720
atctaaagat aaggactttt ccattgatat tataaaaagc actcatgacc attggaaaagc780
attagtgact aagaaaacgaa atggaaaaag gatcatgttg attgttcaac tttcggtgg840
gccccctcaaa gtgtgc                                         856

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(2) INFORMATION ON SEQ ID NO. 53:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 540 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

gatatagacaa agggcctca gatcgcgca ggcgaattgt gccctggttc gccaagatgt 60
cggtcccaa gtataagccg tcgagcctgc gcactctgcc tgagaccctc gacccagccg120
aataacaacat atctccggaa accccggcgaaa cgcaagcgag cgggtggcca taagagccc180
gctgaaacga gagtacctgc ttcaagtacaa cgatccaaac cgccgagggc tcatcgaaaa240
tcgtccctg cttegttggg cctatgcaag aacaataaat gtctatccta atttcagacc300
caatcctaaa aactcactca tgggagctc gtgtggatggccccctca tcttcattta360
ttatattatc aaaactgaga gggataggaa agaaaaactt atccaggaag gaaaattgga420
tcgaacattt cacctctcat attaaagtctg gcaatgatga ctatatgtat tcctgcctaa480
ataaatcatc tattaatcat taaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaagtgc540

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1912 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

tgtgtgaggg ccaacagcgg aatcatcgat gcaggggcct gaattaatgt atctgtgatg 60
ttacagccct tcgattatga tccccatgag aaaagtaaac acaggatgtatg gttcatgtcta 120
tgtttgcctt aactgacact tcagatatgg aaggcgtatg gaaggaggcga aaaccggaag 180
accttatgga ttcaaaaactt agatgtgtt ttgaattgcc agcagagaat gataaaccac 240
atgatgtaga aataaataaa attatatcca caactgcacaa aagacacagaa acaccaatag 300
tgtctaagtgc tctgagttct tctttggatg acacccaaatg taagaaggtt atggaagaat 360
gtaaaggct gcaagggtgaa gttcagggc tacgggagga gaacaagcag ttcaaggaag 420
aagatggact gcggatgagg aagacagtgc agagcaacag ccccatttca gcattagccc 480
caactgggaa ggaagaaggc ctttagcaccc ggcttgcgc tctgggtgtt ttgttctta 540
tcggtgggtt aattattggg aagattgcct ttagaggtt gcatgcacag gatggtaat 600
tggattgggtt gatccaccat atcatgggat taaaatttat cataaccatg tgtaaaaaaga 660
aattaatgtt ttagacatc tcacaggctt tgcctttaaa ttacccctcc ctgcacacac 720
atacacagat acacacacac aataataatg taacgatctt ttagaaagtt aaaaatgtat 780

atgttaactgtat tgagggggaa aagaatgtat tttataatg acaaggggaaa ccatgagtaa 840
tgcacaaatg gcatatgtt aatgttcattt taaacattgg taggccttgg tacatgtatgc 900
tggatrtacct ctcttaazat gacacccttc ctgcctgtt ggtgtggcc cttggggagc 960
tggagcccaag catgttgggg agtgccgtca gtcacacaca gtatgtccca cgtggcccac1020
ccccggccca ggcttgcctt cgtgttccca gttctgttca agccatcage tcttgggac1080
ttagaaacaa agtcagaagc cttttttttt gactgtatgtt cttttttttt tggcaatgtt1140
ataagtttggaa ggcgtgtttt gactgtatgtt cttttttttt tggcaatgtt1200
ttgttcaactt aaaggggacca agctaaattt gtattggttc atgttagtggaa gtcaaaactgtt1260
tatttcagaga tggttaatgc atatttact tattttatgt atttcatctc atgttttctt1320
attgttccaaa gagttacagtt aatgttgcgt gtcgttgcac tctgttgggtt gaaactggat1380
tgcgtgttggaa gggctgtggg ctccctgttgc tctggagagt ctggcatgtt ggaggtgggg1440
tttattttggaa tgctggagaa gagcttgcac gaaatgtttt ttctgggtca gtaaaataac1500
actgttcatag ggaggggaaat tcttgcgttgc gacagtcaac tcttaggttac cttttttttt1560
gaagaatgtt cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt1620
cagcggcccaag gtccaaatgtt gggcttgcac tcccttggg gaccttgcct ggagtccagg1680
caaataatgtt gggcttgcac ggggtttagaaag cgagggttgc accgttgcgtt ggtggggagc1740
aaagggaagag agaaaactttt cttttttttt tttttttttt tttttttttt tttttttttt1800
atataattttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt1860
gaaaaattttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt1912

(2) INFORMATION ON SEQ ID NO. 55:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vi) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

tttttttttt	tttatcggag	caagaatctg	ttaacagttt	tatTTTTTTT	tatgttaat	60
accatgggac	aggattgtaa	ggataaaaaa	ctcagtcaac	aactgcctca	caaggataa	120
aaaaaaattct	gccatgatat	tagcaaagg	aaaggaggaa	aaatttacac	tgtaagaggc	180
accatTTCCC	caaggaatac	ctcttggcat	ttcttgaatg	agtgggatta	gcaatctaaa	240
taaatcatat	ttcaagaggt	aacagcaaca	gataaaaattt	aaagggatta	ttaaaataac	300
atttacaaga	ctctgaacaa	ttcttgaact	cttattaaaa	ccacaaagaa	agacaattc	360
tttattttag	aatttcataa	aggactcaat	gtcaactga	catctgctag	tgatgatctg	420
gtaatataca	acctgtccag	tagccgaaca	gtttgttttt	attgtgtttt	ctaaccgtaa	480
gagatcatta	aaggcaaagc	ctatatgacg	ctgtacacac	aaaaaaatgg	tcaccgtggg	540
ccatactacc	aatgaaatgg	taggtaaaca	aatcttttc	tggtaaagag	aaaaaaaaaa	600
aaaagaaaaca	gcactctgca	tgcttcactc	tacaagatga	atttccctag	aaagaatcca	660
atgaaaatgg	ctgcattttac	aacaagaagt	gaaggaaagag	gactgggtac	attatctctg	720
aaggatcgag	ttgagggtga	tccagggtta	tccgaatgtg	ctaccccttct	gaggccttaaa	780
ccttccatctc	tcaggtgccc	attttcttct	gatagcttca	tcattttctcc	ctgaagtctt	840
tttacacttt	ccatattgtt	ccttggttcg	gtatcattaa	gtgaaaacact	gtgtgggtt	900
ggcatacgtc	cattttgttt	agatgcattc	agtggaaacag	cttgtctagg	ttccatataca	960
ttcaattttat	cattttcatt	gggcatttca	aatacgcattc	tcaattttga	atccattataat	1020
tcatcagggt	ttgcctcttt	ccacacagct	tccatatactg	aagtgtttgg	tggagcaaaa	1080
atgtctgtt	ccataaaactt	gtgtttactc	ttttcattcg	gatcatagtc	aaagggtctgtl	1140
agsattactg	aaacagtcac	agttgaccct	gggtcaataa	ttccactgtt	gggcctcacal	200
cagtacccgc	gagggtctgt	agttttcaact	ttgaaaacaca	cttttctatc	cgatggattt	1260
cgcaattttaa	gattttgtgt	gactacatct	gtgaaggggc	ctttgaattt	gagggtctgtgl	1320
ggcggatcga	ggaccaggat	ctgcicgtct	tcgccccatggc	ccctgaggcg	gacgccccatcg	1380
gagagacagc	gcagagcagg	gggggggttgg	ctcgctgggg	gcggggggacg	atggcgagag	1440
gggaggggga	gcfagttcgc	atcttctctt	ttcttgggtt	gactctgttc	aaccacattcl	1500
ttatgtttggc	agatctgttt	ccagattttat	ttttagagca	ccatctactt	cacatttctgtl	1560
atctctgattt	tgtttttttt	tgtttttgggtt	ttcttgaatct	taaaatgtctg	ccccggaaaat	1620
actatattat	ttagttttgt	ttcttggatggc	ctccgtctgt	ctggatcttt	ggggggaaaat	1680
acaggatctt	tcagactgt	gggttttttttt	atttgcatttt	agcaatgcac	tttttttcttaa	1740
atatggggat	atttaccttt	attaagaaat	tataactaaac	atttgcatttt	tttgcatttt	1800
tatgttctca	tattactttt	gatttctacta	tgatttgcattt	gtgggtgaaca	aagatcattaa	1860
caaacaaaaaa	ctgtatattt	gttataattt	atttgcatttt	atttgcatttt	aaaataaaag	1920
ctaaaaatgt	aaaaaaa	aaaaaaa	aaaaaaa	aa		1962

(2) INFORMATION ON SEQ ID NO. 56:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1458 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

- (vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

cggctcgagc ggctcgagat tcgaggctcggt ggtggcttg gaagagcgtc gagggggccg 60
 tggacgtgga atggggccgag gagatggatt tgattctcggt ggcaaactgtg aattttagat 120
 gcatagtggaa agtgatagat ctggcctgaa gcacgaggac aaacgtggag gttagcggatc 180
 tcacaactgg ggaactgtca aagacgaatt aacagagtcc cccaaataaca ttcagaaaaca 240
 aatatcttat aattacagtg acttggatca atcaaatgtg actgaggaaaa cacctgaagg 300
 tgaagaacat catccagtgg cagacactga aaataaggag aatgaaggtaa aagaggtaaa 360
 agaggagggt cccaaagaga tgactttggta tgagtggaaag gcttattcaaa ataaggaccg 420
 gcacaaaagta gaatttaata tccgaaaacc aaatgaaggt gctgatgggc agtggaaagaa 480

gggattttgtt cttcataaaat caaagagtgaa agaggctcat gctgaagatt cggttatggaa 540
 ccatttttc cggaaagccag caaatgatata aacgttctcgat ctggagatca attttggaga 600
 ccttggccgc ccaggacgtg gccccggagggt ggacgtgggc gtgggtggcg 660
 cccaaaccgtt ggcagcggaa ccgacaaggc aagtgtttct gcttctgtat tggatgaccc 720
 aaggaggatcc ccagctctgg cttaaactggta tgccataaga caaccctggat ttctttgtga 780
 acccttttgtt tcaaaagcttt tgcatgttta aggatccaa acgactaaga aattaaaaaa 840
 aaaaagactg tcattcatac cattcacacc taaagactga attttatctg ttttaaaaat 900
 gaaccttctcc cgctacacag aagtaacaaa tatggtagtc agttttgtat ttagaaatgt 960
 attggtagca gggatgtttt cataattttc agagattatg cattcttcat gaataactttt1020
 gtatttgcgtt ttgcaaatat gcatttccaa acttggaaata taggtgtgaa cagtgtgtac1080
 cagtttaaag ctttcaatttcc atttggttt tttaattaag gattttagaaat ttcccccaat1140
 tacaaaactgg tttaaatat tggacatact ggttttaata cctgctttgc atattcacac1200
 atggtaact gggacatgtt aaactttgtat ttgtcaaattt ttatgtgtg tggaaatacta1260
 actatatgtt tttaactta gtttaataat tttcatttt gggaaaaat ttttttcac1320
 ttctcatgtat agctgttata tatatatgtt aaatctttat atacagaaaat atcagactt1380
 gaaacaaatc aaaagcacat ttggtttatt aaccctgtggc tggccctggca tggggcccat1440
 ttgggggtcca aattataa 1458

(2) INFORMATION ON SEQ ID NO. 57:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2188 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

ggggccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc 60
cccccccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc 120
cccccccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc 180
cccccccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc 240
cccccccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc cccccccccccc 300
ccaacccctcc cccacccccc cccctacaag tcacctgggt aagccaaacct gaattctact 360
cacctggcg tggaaagtatg tatgacagaaa tgccgacgagg aggtgatgga tatgatggg 420
gttatggagg ttttgatgac tatgggtggct atataaatta cggctatggg aatatgggt 480
ttgatgacag aatggagagat ggaagaggta tgggaggaca tggctatggt ggagctggg 540
atgcaagttc aggtttcat ggtggtcatt tcgtacatata gaggagggtt cttttcgtg 600
caactgaaaa tgacattgtc aatttcttct caccactaaa tccaaatacga gttcatattg 660
atattggagc tgatggcaga gccacaggag aagcagatgt agagtttgt acacatgaag 720
atgcagtagc tgccatgtct aaagataaaaa ataacatgca acatcgatat attgaactct 780
tcttgaattc tactccttggc ggcggctctg gcatgggagg ttcttggaaatq qgaggctacg 840

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(2) INFORMATION ON SEQ ID NO. 58:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1548 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

- (vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

ctcgcttagtt cgatcggtag cgggagcggga gagcggaccc cagagagccc tgagcagccc 60
 caccgcggcc gcccggcttag ttaccatcac accccggggag gggccgcagc tgccgcagcc 120
 gccccccagtc accatcacccg caaccatcgag cagcggaggcc gagaccccgac agccgcggcc 180
 gccccccccc gggggccccc ccctcagcgc cggccgacacc aagcccgccaa ctacggcag 240
 cggcgcaggg agcggtgcc cgggcggcc cacatcggcg gcccctgccc gcggggacaa 300
 gaaggtcatc gcaacaagg ttttgggaac agtaaatgg tcaatgtaa ggaacggata 360
 tggtttcatc aacagaatg acaccaagga agatgtatgg gtacaccaga ctgccataaa 420

aaagaataac cccaggaagt accttcgcag tgttaggagat ggagagactg tggagtttga 480
 ttttgttcaa ggagaaaagg gtgcggaggc agcaaatgtt acaggtcttg gtgggtttcc 540
 aatccaaggc agtaaatatg cagcagaccc taaccattat agacgctatc cacgtcgttag 600
 ggggttcctcca cgcaatttacc agcaaaaatta ccagaatagt gagagtgggg aaaagaacga 660
 gggtatcgagg agtgctcccg aaggccaggg ccaacaacgc cggccctacc gcaggcgaag 720
 ttcccccaccc tactacatgc ggagacccta tgggcgtcga ccacagtattt ccaaccctcc 780
 tggcgtggcga gaagtgtatgg agggtgtctga caaccagggt gcaggagaac aagtagagacc 840
 agtgaggcag aatatgtatc gggatatacg accacgattc cgcaggggcc ctctcgcca 900
 aagacacccct agagaggacg gcaatgaaga agataaaagg aatcaaggag atgagacccca 960
 aggtcagcag ccacctcaac gtcggtaccg cgcgaacttc aattaccgac gcagacgccc 1020
 agaaaaacccct aaaccacaaag atggcaaaga gacaaaagca gccgatccac cagctgagaal080
 ttsgtcccgcccggctg agcaggccgg ggctgagtaa atgcccgtt accatctctall140
 ccatcatcccg gtttagtcat ccaacaagaa gaaatatgaa attccagcaa taagaaatgaa1200
 acaaaaagatt ggagctgaag acctaaatgtg cttgcctttt gcccgttgcac cagataaaata1260
 gaactatctg cattatctat gcagcatgg gttttttaaa ttttaccta aagacgtctc1320
 tttttggtaa taacaaacgt gttttttaaa aaagctgtt ttttctcaat acgccttaa1380
 aggtttttaa attgtttcat atctggtcaa gttgagattt ttaagaactt catttttaat1440
 ttgtataaaa agtttacaac ttgatTTTTT caaaaaagtc aacaaactgc aagcacctgt1500
 taataaaaggctttaaataat tgtctttgtg taaaaaaaaa ggaaatat 1548

(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1254 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ggaccgcttc ccccgagcca gcagcagcgt ttgacgtcat cgtgcgtgtg gtgcccctgc 60
tgccggggct ggtgatttga gggaaaccccg tggctgtacgg agggctgttag cctgtgagca 120
gcgagatcca gggacagagt ctccagcctcg ccgctgtgc cgccgcccgc gccccagagac 180
tgctgagccc gtccgtccgc cgccaccacc cactccggac acagaacatc cagtcatgga 240
taaaaatggaa ctggttcaga aggccaaact ggcccggcag gctgagcgat atgatgacat 300
ggcagcctgc atgaagtctg taactgagca aggagatgtaa ttatccaaatg aggagaggaa 360
tcttctctca gttgcttata aaaatgttgtt aggagccctgtt aggtcatctt ggagggtcgt 420
ctcaagtatt gaacaaaaga cggaaagggtgc tgagaaaaaa cagcagatgg ctcgagaata 480
cagagagaaa attgagacgg agctaagaga tatctgcaat gatgtactgt ctcttttgg 540
aaagttcttg atccccaaatg ctccacaagc agagagccaa agtcttcttat ttgaaaatga 600
aaggagatta ctaccgttac ttggctgagg ttgccctgtt tgatgacaag aaaggattt 660
tcgatcgttc acaacaagca taccaagaag cttttggaaat cagaaaaaag gaaatgcaac 720

caacacatcc tatcagactg gggctggccc ttaacctctc tgggttcttat tatgagattt 780
tgaactcccg cagagaaaagc ctgtctctt gcaaagacag cttttgtatga agccattgtt 840
gaacctgtata cattaagtga agagtataac aaagacagca cgctaataat gcaattactg 900
agacacaaact tgacattgtg gacatcggtt acccaaggag acgaagctga agcaggagaa 960
ggagggggaaa attaacccgc ctcccaactt ttgtctgcct cattctaaaa tttacacagt1020
agaccatttg tcatccatgc tggcccacaa atagttttt ttgttacgtt tatgacaggt1080
ttatgttact tcttatttggaa ttcttatatt ttccctgtgg tttttatgtt tagtttggg1140
ggagtagggag ccagttaac gtttggggag tttgtgttt ttctgtcttt gaggggtggg1200
ccagtatggg ggggtgttgg gattttttgtt taccagggtt tgaggtgttt ttgg 1254

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(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 954 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

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cctctttttt ttctttttct tctttttttt ttcctttttt ttttttgtga gaggcagggtc 60
actttatgg tatagagact gcagagggac caggggcttt agctgttgc agctatggtg120
tccttaatcc agtccacata gttgttagacc ttgtgttaga ctccaggcct gttttctgg180
gcacagccat agccccagga gacaatttct tggagctctc cattggagac cacagggcca240
ccagaatcac cctggcagga atccttgctt ccctcgagga agcccacaca gaacatgttg300
ttggtaatct ttccagggtt ggaggctca cactcagcct ggctcagcac aggagcatcc360
aggcactgca gctcgtctgg gtagtcggca ccagaactca gagtgttgcc ccagccggag420
atgagggact cggtgccagc agctggaggg gcagtgggca gagagatggc ggacacgccc480
gaattgtga cggcaggtga ggagagctt atcagcagga tgcattgtc cagagtccgg540
ctgttgtatt tggggtgtgcg gatgatctt gcccatttga tgaactgttc attccctcc600
aggacttcga tgggtgtctc tcccaatctc acctggatgc gggacttgttga gcagtgacct660
gctgacacca cccactgttc gctgatgagg gagccaccgc agaagtggta gccagaattc720
aaggacacct ggtaggggac agaattctcc tcacagatgt agcccccaac gatcttgtca780
tcatcatcaa agggggcagc aacagcagct gcaacaaaagg taaggatcag aagtagattc840
atggtggtag agtgtgcctg attgctggtg gagaacccgt ctttataacct cccgaggatg900
gggagaggag gtgtctgtga ggtgagggtc actgctcctc ccagcaca caca 954

```

(2) INFORMATION ON SEQ ID NO. 65:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2213 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

ggcgggaccccg ccggggggctcg aggccgtgcct ctccgagaga tcctggcgcg gccgtcccgg 60
 cccggggccc cagggtgcgt tccccatagag agggattttc cggtctcggt ggcagagggaa 120
 caaccaggaa cttgggggctc agtcttcacc ccacagtggg gcggatccgt cccggataaag 180
 acccgctgtc tggccctgtag tagggtgtga cttccgcagc cgagaggag gagcgcagcc 240
 ggctctgaag aacttctgt tgggtggctg aactctgtat ttgacctaga gtcatggcca 300
 tggcaaccaa aggaggtact gtcaaagctg cttcaggatt caatgccatg gaagatgccc 360
 agaccctgag gaaggccatg aaagggtctg gcaccgtat agacgccatt attagcgicc 420
 ttgccttaccg caacaccgcg cagcgcagg agatcaggac agcstacaag agcaccatcg 480
 gcaggagactt gatagacgac ctgaagtcaag aactgagtgg caacttcgag caggtgattt 540
 tgggatgat gacgcccacg gtgtgtatg acgtgcaaga gctgcaagg gccatgaagg 600
 gagccggcac tgatgaggc tgccttaattt agatcctggc ctccggacc cctgaggaga 660
 tccggcgcat aagccaaacc taccaggcgc aatatggacg gagccttggaa gatgacattc 720
 gtcgtacac atcggttcatg ttccagcggag tgcgtgtgtc tctgtcagat ggtgggaggg 780
 atqaaggaaa ttatctggac gatgtctcg tgagacaggta tgccaggac ctgttatgagg 840
 ctggagagaa gaaatggggg acagatgagg tgaaattttt aactgttctc tttttccggga 900
 accgaaatca cctgttgcat gtgttgtatg aataaaaaag gatatcacaag aaggatattt 960
 aacagagtat taaatctgaa acatctggta gctttgaaga tgctctgtc gctatagtaa1020
 agtgcgtatgag gaacaaatct gcataatttt ctgaaaagct ctataaatcg atqaagggtct1080
 tgggcaccga tgataaacacc ctcatcagag tgatggtttc tcgagcagaa attgacatgt1140
 tggatatccg ggcacacttc aagagactct atggaaagtc tctgtactcg ttcatcaagg1200
 gtgacacatc tggagactac agggaaatgtc tgcttggatc ctgtggagga gatgattaa1260
 ataaaaatcc cagaaggaca ggaggattct caacactttt aatttttttta acttcattt1320
 tctacactgc tattatcatt atctcagaat gtttttttcc aattaaacg cttacagctg1380
 cttccatgaa tataactgt ctgttattt attcacatcatt aattgtcat tatgtgtctt1440
 taaagctgta cttgcatttc aaagcttata agatataaat ggagatttta aagtagaaat1500
 aaatatgtat tccatgtttt taaaagatta ctttctactt tggatccac agacattgaal1560
 tatataaaat tattccatat ttctttca gtggaaaatt ttttaatgg aagactgtt1620
 taaaatcact ttttcccta atccatattt taggtggct agtagtttct tcatttgaal1680
 ttgttaagcat cccgtcgtt agaatcccc tccagttttc tatatttcat agtcaaagcc1740
 ttgaaagcat ctacaaatct ctttttttag gttttgtcca tagcatcgt tgatccttac1800
 taagttttc atgggagact tccttcatca catcttatgt taaaatcact ttctgtgtc1860
 aaagtatacc aaaaccaat tatctgaact aaattctaa gtatggttat acaaaccata1920
 tacatctgtt taccacaaatc aaatgtgtt cattccatatt tattatagtt aatgtcttaa1980
 tccagcttc aagtgaatgg aaaaaaaaaat aagcttcaaa ctaggttattc tggaatgtat2040
 gtaatgctct gaattttgtt tgatataaaag aaaactttttt tggatccatc tttttttta2100
 aaatcaattt ttgttggatgtt agtaatttttctt attgcactt tggatccatc cttccagaaac2160
 attctgaaga tgtacttggaa tttataaaaa aagttcactt tgtaaaaaaaa aaa 2213

(2) INFORMATION ON SEQ ID NO. 67:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2878 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

cctcgtgcac gtgcaccgcgt tggtcctaaa agctctggag gatggccccc .catatgggtc 60
 tccatgggc aacaaacaga tcacaagggtg cctaattgaa tgtcagatg aataataata 120
 taatgtggag gctgtggagc tgctaattcg caatcatttg gtaatatgc agcagtatga 180
 tcttcaccta gcgagtcaa tggagaatgg cttaaactac atggctgtgg catttgcstat 240
 gcagtttagta aaaatcctgc tggtgatgaa aaggagtgtt gctcatgta ctgaggcaga 300
 tctgttccac accattgaaa ccctcatgag gattaatgct cattccagag gcaatgctcc 360
 agaaggattg cccccagctga tggaaagtgt gcgatccaac tatgaagcaa tgattgatcg 420
 tgctcatgga ggcccaaact ttatgatgca ttctggatc tctcaaggct cagagtatga 480
 tgacccttca ggccgtgggg agaaggcaga gtatcttctg agggaaatggg tgaatctcta 540
 ccattcagca gcagctggcc ggcacagtac caaagcttc tctgcatttgg ttggacagat 600
 gcaccagcaa ggaatctgaa agaccgtga tctcataaca aggttcttgc gtcgtgtac 660
 tggaaatgtgt gttgaaatca gttaccgtgc tcaggctgag cagcagcaca atccctgctgc 720
 caatccccacc atgatccgag ccaagtgtct tcacaacactg gatgccttgc ttgcactct 780
 tgcactgctc gtgaaacact caggggaggg caccAACACT gtcacaaaga ttaatctgt 840
 gaacaaggtc ctgggtatag tagtgggagt tcttccttcag gatcatgatg ttgcctcagag 900
 tgaatttcag caacttcctt accatcgaaat ttttatcatg cttctcttgg aactcaatgc 960
 acctgagcat gtgttggaaa ccattaattt ccagacactt acagcttct gcaatacattl020
 ccacatcttgc aggccatcca aagctcttgc ctttgtatata gctggcttgc aactgatttc1080
 ccatcgatata ttattgcaa gaatgctggc acatacgcca ctttcctta gaaatgtggal200
 gtatgcacag ctactgattt atttattcaa atatttagcg agagtgtgc tgggtctttt1260
 actcacaaaaa cctatgcaaa tcctctacaa gggacttta ttctgtatg tgatcccaccl320
 gcatgatttcc cagaggttcc ttgtgatta ccattatggg ccaagaaaca tgaggctcccl380
 taattgtatc cagttaaagaa atttgatctt gaggcctt ccaagaaaca tgaggctcccl380
 cgaccatccatc acttcataatc taaaggtgga catgttgagt gaaattaaaca ttgctcccg1440
 gattctcacc aatttcactg gagtaatgcc acctcagttc aaaaaggatt tggattccctal500
 tcttaaaact cgatcaccatc tcacttctt gtcgtatctg cgcagaaacct acaggatcccl560
 aatgaacactg ggaatcgta caacccatcgat ctcatcaatg cactgggtct ctatgtccgg1620
 actcaggccatc ttgcgcacat ccacaacaag ggcagcacat cttcaatgag caccatcactl680
 cactcagcac acatggatat cttccagaat ttggctgtgg acttggacac tgagggtcgc1740
 tatcttttt tgaatgcaat tgcaaatcag ctccggtacc caaatagcca cactcactac1800

(2) INFORMATION ON SEQ ID NO. 68:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 701 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vi) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

atgatatttt ggatgttagtc ttttgattgt taaaatctta aaaagttaatg ggatcttttg 60
acactgggtt atgttttatt ttatgtgtg caaatttaa ccatattctt ttctagttaa120
agaggaaaaa gcaagttgct ccagaaaaac ctgtaaagaa acaaaaagaca ggtgagactt180
cgagagccct gtcatcttct aaacagagca gcagcagcag agatgataac atgtttcaga240
ttggggaaat gagttacggtt agtgttcgcg attttaaagg caaagtgccta attgatatta300
gagaatattg gatggatcct gaaggtgaaa tgaaaccagg aagaaaaaggt atttctttaa360
atccagaaca atggagccag ctgaaggaac agatttctga cattgatgat gcagtaagaa420
aactgtaaaa ttcgagccat ataaataaaa cctgtactgt tctagttt ttaatctgtc480
tttttacatt ggctttgtt ttctaaatgt tctccaagct attgtatgtt tggattgcag540
aagaatttgt aagatgaata cttttttta atgtgcatta taaaaatat tgagtgaagc600
taattgtcaa ctttattaag gattactttg tctgcccacc accttagtgta aaataaaatc660
aagtaataca atcttaaaaaa aaaaaaaaaa aaaagtcgag c 701

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 817 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

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gttttttttt tttttttttt ttttttttaa gcacagaaaag cttttattac cacagaggaa 60
atcaggaaat gctggaggca gcctcgtag ctgtgtgatc agggagggga cagcagggcg 120
gaacccgtca tcaatcatgt ctgggcagtc tcccaaccaa caggtttgtt tggttcagg 180
gaggcttttg ctgggcgttg tgggtgtatc atcaggaagg tcagcctcaa caaatgggct 240
tcttcctgga cataggacag ccagaatcgg ggacaccagc tgacagaca ccaccta 300
atggaaatca aatttaggttc attacatca gaaatgtatc tcaccctgat cataaaagag 360
ggacaaggaa gcactggct ctactggata gcctttctt tagataagat gctttaaaa 420
gttaaacatt ggcaggccct ttccccttagc taacagcaag cagcacacaa ttccaagtca 480
gcttgtaaag cttttgttat ctttggatc tggttattt tggttttgta acgaaattga 540
tggagtacga gccggtagag gaatcctgtt tgatctggaa atttccgtg gagagccaa 600
aagggtcgag aaccaagttc ccaagatctt ttaatttacc taacatctt tcttttagtc 660
tttcatttacg ttcttcaatt tgcttaggtt atctcataca agcttctt gcttgatgt 720
ttgatgaagg ttcccgcctg ctgtccccctc cctgatcaca cagctaacga ggctcccca 780
gcatttcctg atttcctctg tgtaataaaa agctt 817

```

(2) INFORMATION ON SEQ ID NO. 70:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2686 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

gcaaggccta ctgtcggtcg ggaggggagg ttagcccggt ctttgggggt aggcggtagt 60
ggcggaaagag gttcgccgac tgatggcgga tcaggatcg aagcctgcgt aacttttc 120
cttgcattccg gagtcattcc actggatca caatgacatc cttcaagaa gtcccattgc 180
agacttccaa cttgccccat gicatcttc aaaatgtggc caagagtac cttcttaatg 240
cacaccttggc atgtcattac accttaactc catatattca tccacatcca aaagattggg 300
ttggtatatt caagggttggc tggagtactg ctcgtgatta ttacacggtt ttatggtccc 360
ctatgcctga acattatgtg gaaggatcaa cagtcattg tgcactagca ttccaaggat 420
attaccttcc aaatgtatgt ggagaattt atcagttctg ttacgttacc cataagggtg 480
aaattcgtgg agcaagtaca ctttccagt ttcgagcttc ttctccagtt gaagagctgc 540
ttactatggc agatgaaggg aattctgaca tggtagtggt gaccacaaaa gcaaggcttc 600
ttgagttgaa aattgagaaa accatgaaag aaaaagaaga actgttaaag ttaattggcc 660
ttctggaaaa agaaacagca caacttcgag aacaagttgg gagaatggaa agagaactta 720
accatgagaa agaaagatgt gaccaactgc aacgacaaca aaagggtctt actgaagtaa 780
cacaagctt aaaaatggaa aatgaagagt ttaagaagag gttcagtgat gctacatcca 840
aagcccatca gcttgaggaa gatattgtgt cagtaacaca taaagcaatt gaaaagaaa 900
ccgaaattaga cagtttaaag gacaaactca agaaggcaca acatgaaaga gaacaacttg 960
aatgtcaat ggagacagag cttatgtcag aggtccagac taaggatcat ttgaaagaata 1020
cagaaataga aaataccaaag catttcaaaag aagagattgg tttaaaaat tttagtgggat 1080
acaaagaaag cgtgattact cttcaatgc tgcattacaac caggctgcag ttatgttgg 1140
ctgaaaagga aaatctgcaa gtaacttcc tgcttacaac ctcaagtaaa gaagatactt 1200
qtttttaaa ggagcaactt cgtaaagcag aggaacaggt taaggcaat cgccaagaag 1260
ttgtcttctt ggctaaagaa ctcagtgtatg ctgtcaacgt acgagacaga acgatggcag 1320
acctgcatac tgcacgcttg gaaaacgaga aagtaaaaaa gcagtttagt gatcagtggl 1380
cagaacttaa actaaatgtc atgaaaaaaat atcaggacaa gactgatata ctgaaacacg 1440
aactaagaag agaagttgaa gatctgaaac tccgttctca gatggctgca gaccattata 1500
aagaaaaatt taaggaatgc caaaggctcc aaaaacaaat aaacaaactt tcagatcaat 1560
cagctaataa taataatgtc ttccacaaaga aaacggggaa tcagcagaaa gtgaatgtgl 1620
cttcagtaaa cacagaccca gccacttctg cctctactgt agatgtaaag ccatcacctt 1680
ctgcagcaga ggcagattt gacatagtaa caaaggggca agtctgtgaa atgaccaaag 1740
aaattgcgtc caaaacagaa aagtataata aatgtaaaca actcttgcaag 1800
caaaatgca taaaatatgtc gatgaacctg caaaaatggc gctgaaatgg aaagaacaag 1860
tgaaaaattgc tgaaaaatgtc aaacttgcac tagtgcgtt acaggacaat tataaagaac 1920
ttaaaaggag tctagaaaaat ccagcagaaa gaaaaatggc agatggagca gatggtgctt 1980
tttacccaga tgaataacaa aggccacctg tcaaggtccc ctcttgggaa ctgaaagaca 2040
atgttgtcg cagccagct gtcgaaactt ttagtccggcc tgatggctt gaggactctg 2100
aggatagcaa agaagatggc aatgtgcata ctgcctctga tcctccaatgt caacattttac 2160
gtgggcatgg gacaggctt tgcttgcattt ccagcttgc tcttccaaatg aatgttcccc 2220
tctgtgagtt aatgtttctt ctaactatg atcagagcaa atttgaagaa catgtgaaa 2280
gtcactgaa ggtgtccccg atgtgcagcg aacgatccc tcctgactat gaccagcagg 2340
tgtttgaag gcatgtgcag acccattttg atcagaatgt tctaaatttt gactagttac 2400
tttttattat gatgtatata agtttagcag taaaaaaaaa aaaaaaaaaacc acacctaataa 2460
tagaccactg aggagaccat agagcggatg ctttcatgca cccttactg cactttctga 2520
ccaggagcta ctttgagttt ggtgttacta ggatcagggt cagttttgg cttatcaata 2580
aattttaaat tctgttaatc ttacccaaat taaaaaaaaa aaaaaaaaaat cgtactttat 2640
ttatccctag ttgcagactg ctgaataaaag gtcaaggatt atccat 2686

(2) INFORMATION ON SEQ ID NO. 72:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 922 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

- (vi) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ctgctctgaa aagccatctt tgcattgttc ctcatccgcc tccttgctcg cggcagccgc 60
ctccgcgcgc cgccctccccc gcccggcgg actccggcag ctttatcgcc agagtccctg 120
aactctcgct ttcttttaa tccccctgcat cggatcacccg gcgtgcggca ccatgtcaga 180
cgcagccgta gacaccagct ccgaaatcac caccaaggac ttaaaggaga aagaaggaa 240
tgtggaaagag gcagaaaatg gaagagacgc ccctgcta ac gggaatgcta atgaggaaaa 300
tggggagcag gaggctgaca atgaggtaga cgaagaagag gaagaagggg ggtgatggtg 360
aggaagagga tgagatgaa gatgaggaag ctgagtcagc tacggcaag cggcagctg 420
aagatgatga ggatgacgat gtcgatacca agaagcagaa gaccgacgag gatgactaga 480
cagcaaaaaa gggaaaatgta aactaaaaaa aaaaaggccg ccgtgaccta ttccccctcc 540
acttcccgtc tcagaatcta aacgtggta cttcgagta gagagggccg cccgcccacc 600
gtgggcagtg ccacccgcag atgacacgcg ctctccacca cccaaaccaa accatgaga 660
tttgcaacag gggagggaaa aaggacaaa acttccaagg ccctgctttt tttttttaaa 720
gtactttaaa aaggaaattt gtttgatgt tctatttaca ttgtatgtg ttgtacatat 780
tgttaggggt caaccatttt taatgatctc ggatgaccaa accagccttc ggaagcggtc 840
tctggcctac ttctggactt ttacgttgg ggttgttga ccatgttcaa ttataatccc 900
aaaaggggga aaaaaaacct tt 922

(2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 870 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

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ggaactggcg gtgcgagggc tgctgcacag cgagcggagc cgcggccgg acggcagcgc 60
gtcccccgag ctcccccct ccccccggcc gccagccgag gcagctcgag cccagtccgc120
ggcccccaga ca gca gcccga gagcagcccc agtagcagcg ccatggccgg gtggAACGCC180
tacatcgaca accctcatggc ggacgggacc tgcaggacg cggccatcg gggctacaag240
gactcgccct ccgtctgggc cgccgtcccc gggaaaacgt tcgtcaacat cacGCCAGCT300
gaggtgggtg tcctgggtgg caaagacccg tcaagttttt acgtgaatgg gctgacactt360
gggggcaga aatgttcggat gatccgggac tcactgctgc aggtatgggaa atttagcatg420
gatcttcgta ccaagagcac cggtggggccc cccacccctca atgtcactgt caccAAAGACT480
gacaagacgc tagtcctgct gatggggaaa gaagggtgtcc acgggggttt gatcaacaag540
aaatgttatg aaatggccctc ccacccctcg gttcccaagt actgacccctg tctgtccctt600
cccccttccacc gctccccaca gctttgcacc cttttccctcc ccatacacac acaaaccatt660
ttatTTTGTG ggcattacc ccataccccc tattgctgcc aaaaccacat gggctggggg720
ccagggtgg atggacagac acctccccc accatatacc ctcccgtgtg tggggaaa780
acttttggttt ttgggggttt ttttttctg aataaaaaaaatctactta aaaaaaaaaa840
aaaaaaaaaaaaaa aaaaaaaaaaaaaaa 870

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(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

(2) INFORMATION ON SEQ ID NO. 76:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1712 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

gtggcagaaa acctcatgac acaaactctc cgccctccctg tgggtgttggaa ggatgtctgc 60
 agcagcatt aaattctggg aaggcttggt tgcagcagc agcaggaggg gcagagcaca 120
 gcatcgctgg gaccagactc gtcctcaggcc agttgcagcc ttctcagcca aacgcccacc 180
 aaggaaaaact cactaccatg acaaattgcag tgatttgc ttgcctccta ggcatacac 240
 gtgccatacc agttaaacag gctgattctg gaagttctga gaaaaaggcag ctttacaaca 300
 aataaccaga tgctgtggcc acatggctaa accctgaccc atctcagaag cagaatctcc 360
 tagccccaca gaatgtgtg tcctctgaag aaaccaatga cttaaacaag gagacccttc 420
 caagtaagtca acacgaaagc catgaccaca tggatgatat gatgatgaa gatgatgacg 480
 accatgtggc cagccaggac tccattgact cgaacgactc tggatgatgaa gatgacactg 540
 atgattctca ccagttctgat gatgttcacc attctgatgaa ctggtcactg 600

 attttccac gacccatggca gcaaccqaag ttttcaactcc agttgtcccc acagtagaca 660
 catatgatgg ccgagggtat agtgtgttt atggactgag gtcaaaatct aagaagttt 720
 gcaacccatgaa catccatgtac cctgtatgcta cagacgagga catcacctca cacatgaaa 780
 gcaaggaggtt gaatggtgca tacaaggccca tccccgttgc ccaggacccgt aacgcgcctt 840
 ctgatttggg cagccgtggg aaggacaggat atgaaacgag tcaagctggat gaccagagt 900
 ctgaaacccca cagccacaaag cagtccatgat tatataagcg gaaagccaaat gatgagagca 960
 atgagcatcc cgtatgttgc gatgttcagg aactttccaa agtcagccgtt gatccacal020
 gccatgatattt tcacagccat gaaatgtatgc tgggtgttga ccccaaaagt aaggaagaag1080
 ataaacacccat gaaatttcgt atttctcatg aatttagatag tgcattttctt gaggtaatt1140
 aaaaggagaa aaaaatacaat ttctcaactt gcattttatgc aaaagaaaaaa atgctttata1200
 gcaaaatgaa agagaacatg aatgtcttctt ttctcatgtt attgggttga tggatctt1260
 tttgagtctg gaaataacta atgtgttttga taattttttt agtttggc ttcatggaa1320
 ctccctgtaa actaaaaagct tcagggttat gtctatgttc atcttataga agaaatgcaai380
 actatcaactg tattttataa tttgttatttc tctcatgaat agaaattttat gtagaaagcaal440
 acaaaaatact ttaccact taaaaagaga atataacatt ttatgtcact ataatcttt1500
 gtttttttaag ttagtgtata ttttgttgc attatctttt tgggtgttga ataaatcttt1560
 tatcttgaat gtaataagaa tttgggtgggt tcaattgtt atttgggttttccacggttgt1620
 ccagcaatta ataaaacata accttttttca ctgcctaaaa aaaaaaaaaaaga gaaaagaaaal680
 aaaaagaaaaag aaaaaaagg gaggggagggg ag 1712

(2) INFORMATION ON SEQ ID NO. 78:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

accgcccccg ctgtgggtct cagcagctcg ggcggcgaaa ggggtggcag cggcaaggca 60
 gcccagtttc gccaaggctg tcggcgccgc gcggcccgca ggcacccggc acgcgccttc 120
 cccgcaggca cccggcacgc gcctccccg cccgcacgat gcccaagagg aaggtcagct 180
 ccgcccaggc gcccacaagg aagagccaa gaggagatcg gcgcgggtgt cagctaaacc 240
 tcctgcaaaa gtggaagcga accgaaaaag gcagcagcga aggataaattt ttcaaaaaaa 300
 aaagtgcaaa caaaaaggaa aaggggagca aaggaaaaac aggccgaagt ggctaaccaa 360
 gaaactaaag aagacttacc tgccggaaaac gggaaacga agactgagga gagtccagcc 420
 tctgatgaag caggagagaa agaagccaag tctgatataat aaccatataac catgtcttat 480
 cagtggccc tgcgtccctt ctgtacaat ccagaggaat atttttatca actattttgt 540
 aaatgcagaat ttttagtag ctctagaaaac attttaaga aggagggaaat cccacctcat 600
 cccattttt aagtgtaaaat gctttttttt aagaggtgaa atcatttgct ggtgttttat 660
 ttttttgtac aaccagaaaa tagtgtggaa tattgaatta tgggaggctc tgactgtctc 720

 ggggtgtcagc ttaacattcc acagatgggg ggttagtttt tatatcctat aatacaaagc 780
 atattaaatg gcaatatggg gtcagtcctg cattaaatgt ctgtaaacatt ttaaattact 840
 tctattacca tgggtttttt tagtagaatt gtttctaaa gaaaaccact ctgtgtatcat 900
 ggtctctctt gccagaattt gtcactt gtaacatctt tgcgttagtc ctgtttctt 960
 aataactttt ttactgtgt gtaaagattt acagatttga acatgtatgt tacgtgttgt 1020
 tgagttgtga actgtgtggc cgtatgtaac agctgaccaa cgtgaagata ctggtaactgt 1080
 atagcctttt aaggaaaatt tgcttccaaa tttaagctg gaaagtcaat ggaataactt 1140
 taaaaaaaaaa ttacaataca tggctttttt gaatttcgtt acgtatgtt agatttgtt 1200
 acaaaatttggaa atgtctgtac tgatcctcaa ccaataaaaat ctcagttatg aaaataaaaat 1260
 aaaaaaaaaaaa aaa 1273

(2) INFORMATION ON SEQ ID NO. 79:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2342 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(2) INFORMATION ON SEQ ID NO. 80:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1959 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

gcagttata aataagttt gggagacaaaa tgatacgcac acgagagaag atgaagaaga 60
 tactcaaagt tccaaatctg aagaacatca ttgtactct aatccaatca aagaagaaaat 120
 gactgagtct aagtctcta agtactctga aatgagttag gaaaaacgag ccaaacttcg 180
 taaaatttgag ctcaaagtta tgaagttca ggatgaattt gaatctggaa aaqacctaa 240
 aaaaccaggc cagagtttc aggagcaagt agaacactac agagataaaac ttcttcac 300
 agagaaagag aaqagatgg aaagagaacg agaaagagac aagaaaagata aagaaaaatt 360
 ggaatctcg tccaaagaca agaaggaaaa agatgagtgt actccgacaa ggaaggaaag 420
 gaagaggcga cacagtacat cccccagccc atctcgactt agcagtggta gacgagtgaa 480
 atccccatca cccaaatcg agcgatcaga gcgttcagaa agatctcata aagagagctc 540
 acggtccagg tcatctcaca aagattctcc tagagatgtt agcaaaaaag cccaaagatc 600
 accatcttgtt tcaaggacac ctaaaaggc taggcgatca cggtcttagat ctcctaaaaa 660

atcagggaaag aagtccagat cccagttccag atctccacac aggtctcata aaaagtcaaa 720
 gaaaaacaaa cactgacgta aatttttaag atgtgtcac ttattggaaa tgcgatttgt 780
 ttgtgcctg aacggcttgtt tttttaaaaa aacaaaaaat caaatgaaag agcattcctg 840
 gggtttttg ttgttttgtt tatgcatgtg taaactcatg agcaactgca tctgttagatc 900
 tgcatttgtt ttatatttgtt taaattactt tcattgtggc tatttctcaa gatgaaattt 960
 ttatttgtct aatggatttc atcagaaatg tgataatgg atctgctgac agtagtagt 1020
 ttgttttta ggatgttgtt acttagcaaa aataatacag atgtcttccc ccctttgtt 1080
 gctttgacaa ttgtttagt atttcaaaata aaatctgaac agaaaactat aatgttgg 1140
 ttgtttccca ccgtgtat taaatccctt aaatccctac tgagtttccactactgtt 1200
 tgcttcttat acctgatgca ctttataaagc cccagtgttc aagtagctt agttttat 1260
 ttactaaat gactatccaa attaaggac ctgagactcc tatttgggg tttgctaacc 1320
 atttgcattt gataagttt tcttgggtaa tactaataacc cagatataaa agactaggta 1380
 gatatggcat ggcgtttgt tagtggatg cctggctaa acatttttt cacagaagca 1440
 atatgatttc catacatccaa acccatgttc tgaccaacta cttacttttta gggggaaattt 1500
 aaatatcttt tcattttccctt ttcttattatg aaagaagttt attttgtaaaa caaatttctt 1560
 aacaagggtt ggcattagaa ttctcttggta tgattgttga ctttttataa tcttctgtt 1620
 gctatcttc aaacactggc atcagaatat ttttataag tttgtgttta aacagcttag 1680
 ttggtcccccc ccccccactcc caagagactt gggtttagtt atagctttaa gtaaaaattt 1740
 aaaataaaaat gttttcagg aaacttcgta tctaatggtt tgtaaaatca aggtgcaaa 1800
 agttgatttta aaccatttgc agagttgaac tctattatga aaataaaattt gctacggat 1860
 gaggaagaaaa taaaacttgtt gtaatgttgg tctataataact gctataaata taataaagg 1920
 ttatgttagaa ttgtactgac aaaaaaaaaa aaaaaaaaaa 1959

(2) INFORMATION ON SEQ ID NO. 81:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 3708 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

ggcccttata	tcacgcacgg	tagacaagct	ttttttttt	ttttttttta	cagttataa	60
cacaactttt	attagaaaag	ttatacataa	catagcatca	actatttca	agaacaatat	120
taaaccggat	aagcaacaaa	aaccagacta	acaaaatgtg	taacaagaaa	ctaagtacct	180
ttctaaaatc	aaacattcaa	ttatctacaa	tgtctttta	caaacgggga	aaactccrtg	240
gtttacaggc	acatcatatt	gaatataaaag	ctgcaatagc	aattttatac	aatttaccact	300
ctgaagaaaac	tgaatcatta	aaacagtaat	tacgagttca	caaatttaaa	acatttcaca	360
taattttaaa	ttattgggta	tacactgaag	tctgagttc	aaaagtgatt	tttttttccc	420
acaaaagttt	caacacttaa	gctagaactt	tcaagtgttaa	cttgcctta	aaaagttaaag	480
acatattctg	ataatcataa	cagtcacatg	atttctgtatg	ctatctggtc	tgttaataat	540

(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 3045 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

gtccattgcc caaaaatccgc tatgaaagct tgaccaatcc ccagtaaattt agacctctgg 60
 gaaaagagct gccatattac ccataccca aacaaccaag atcgaactct cactattgtg 120
 gatactgaa ttggaatgac caaggctgac ttgatcaata accttggtag tattcgccaag 180
 tctgggacca aagcgttcat ggaagcttt caggtctggc cagatatctc tatgattggc 240
 cagttcgttgc ttggttttt ttctgtttt ttgggttgcg agaaagtaac tgtgatcacc 300
 aaacataacg atgatgagca gtacgcttgg gagtcctcag cagggggatc attcacagt 360
 aggacagaca caggtgaacc tatgggtcg ggaacaaaag ttatcctaca cctgaaaagaa 420
 gaccaaactg agtacttgg ggaacgaaga ataaaggaga ttgtgaagaa acatctcag 480
 tttattggat atccccattac tctttttgtg gagaaggaac gtgataaaga agtaagcgat 540
 gatgaggctg aaaaaaagga agacaaagaa gaagaaaaag aaaaagaaga gaaagagtcg 600
 gaagacaaac ctgaaatttg agatgttgg tctgatgagg aagaagaaaa gaaggatgg 660
 gacaagaaga agaagaagaa gattaaggaa aagtacatcg atcaagaaga gctcaacaaa 720
 acaaagccca tctggaccag aaatcccac gatattacta atgaggagta cggagaattc 780
 tataagagct tgaccaatga ctggaaagat cacttggcag tgaagcattt ttcagttgaa 840
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 gaaaacagaa agaaaaagaa caatatcaaa ttgtatgtac gcagatgtttt catcatggat 960
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 aactacaaga aattctatga cgagtcttctt aaaaacataa agcttggaaat acacgaagac 1200
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 taatctctgg ctgagggatg acttacctgt tcagttactt acatccctc tgataatata 2100
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 aaagcagagc tagtaatgtt ttttgagttt catgttgggtt tattttcaca gattgggta 2280
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 gacacagaaaa caggaatgca gacaacatgc atccctgcg tccatgtatg acatgtgttc 2940
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 acttaattcc ttggccaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 3045

(2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 2815 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

cagtggccgc	gcaaccagcc	ttcttagggcg	gcggaggagg	ggagtcaaca	tatccaatgg	60
gcaagtcaaca	gtcgtcgatg	ccagcttctt	cttggaaatct	acccagaatg	gaatcctgac	120
aatgatacacag	gacacacaat	gggtgatcca	ttcatgttgc	agcagtctac	aatccagca	180
ccaggaattc	tggacacctc	acctccctca	tttcatcttg	ggggaccacg	agttggacca	240
agagggaaatc	tgggtgctgg	aatggaaaac	ctgcaaggac	ctagacacat	gcagaaaaggc	300
agagtggaaa	ctagcagagt	tgttcacatc	atggattttc	aacgaggggaa	aaacttgaga	360
taccagctat	tacagcttgt	agaaccattt	ggagtcattt	caaatcatct	gattctaaat	420
aaaattaatg	aggcatttat	tgaaatggca	accacagagg	atgctcaggc	cgcagtggat	480
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aaaaaaactgg	ttctgaggat	tccaaacaca	ggcattgtt	tactgaaaaaa	agataaaatcc	900
cgaaaaaaagat	cttactctcc	agatggccaa	gaatctccaa	gtgataagaa	atccaaaact	960
gatgggttcccc	agaagactga	gagttcaacc	gaagtaaaga	acaagaagag	aagtccgggtgl020	
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aggaaccatc agataaaagct gtgaaaaaaag atggaagtgc ttcagcagca gcaaagaaaa1260
agcttaaaaa ggtggacaag atcgagaac ttgatcaaga aaacgaagca gcgttggaaa1320
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attnatgt tccaagtttca aagaaatgt caacatttttta ttccatttca taaaagacaa2040
aaccaatagt gtttttatta ctttcatctg aaacatttcca tgttttatc tgagccttgc2100
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aacgtgagat tggcaatttga aatgcaggta cagttttctg ttaatgtcat gctgttgc2220
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tatcttgcac cagttataat ttttgagatc ttactgcttg tcacttgaat cccgtgattg2400
tcatacatct ctggtataag caacatttga ttttgaagt gtgttagacca tctttccata2460
ttttcaagat gtaattttac atttctgcat tttaaaaca gtttggccat aatcttagat2520
gcacgccttc aattcatgtt cctgcacatg tgacctttgtt gaaacagaaaat ttgcatgtat2580
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gaatgttaac caaaaaaaaaa aacagtgtg gtttttatttgc gctcttaaac tttgtgcata2760
ctttaacaat ttatcgctt taaatctaga gtgaatttctt aaagagctgc cgctca 2815

(2) INFORMATION ON SEQ ID NO. 84:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 3462 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

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ctggatcgta caagaaggga gacaaggacc actgacaaga taaggcctag caggaaacga 60  
agcggtcttt tccgctatct gccgcttgc caccggaagc gagttgcac acggcaggtt 120  
cccqccccga agaagcgacc aaagcgctg aggacggca acatggtgcg gtccggaaat 180
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atggcagctg	ttgtgtgtgt	tatggacgtg	ggcttacca	tgaactaactc	cattccctgg	240
ataaaatccc	catttgaaca	agcaaagaag	gtgataacca	tgtttgtaca	gcgcacagggt	300
tttgtgaga	acaaggatga	gattgcttta	gtcctgtttg	gtacagatgg	cactgacaat	360
cccccttcgt	gtggggatca	gtatcagaac	atcacagtgc	acagacatct	gatgtacca	420
gattttgatt	tgctggagga	cattgaaagc	aaaatccaac	cagggtctca	acaggctgac	480
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ttcagtggaga	gtctgagaaa	actgtgcgtc	ttcaagaaaa	ttgagaggca	ttccattcac	900
tzggccctgccc	gactgaccat	tggctcaat	ttgtctataa	ggattgcagc	ctataaatcg	960
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gatggagaaga	cagacaccct	tgaagactt	tttccaacca	ccaaaatccc	aaatccctcgac1620	
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gccagcttig	aggaagcgag	taaccagtc	ataaaatcaca	tcgaacagtt	tttggatact2040	
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cttttaagca	gtgagttatg	gtgggtgtct	catgaagaaaa	agaccttttg	gcccaatctc3060	
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ggatgggtc	tcctttacta	aataagaaaa	taacaaagcc	tttattctct	tttttcttg3300	
tcctcattct	tgcccttgagt	tccagttcct	cttgggtgt	cagacttctt	ggtacccagtl3360	
cacctctgtc	ttcagcaccc	tcataagtcg	tcactaatac	acagttttgt	acatgtaaaca3420	
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(2) INFORMATION ON SEQ ID NO. 85:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 668 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

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ataggccgg tgctgcctgc ggaagccggc ggctgagagg cagcgaactc atcttgc当地 60
gtacaggagc tcgtgccgtg gcccacagcc cacagcccac agccatggc tggacactgaa120
cggtgaagat gctggcgggc aacgaattcc aggtgtccct gagcagctcc atgtcggtgt180
cagagctgaa ggcgcagatc acccagaaga tcggcgtgca cgccttcag cagcgtctgg240
ctgtccaccc gagcgggtgtg ggcgtgcagg acagggtccc cttggccagc caggcctgg300
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gcaccgtgtt catgaatctg cgcctgcggg gagcggcactc agagcctggc gggcggagct600
aaggcctcc accagcatcc gagcaggatc aaggccggaa aataaaggct ttgtaaaaga660
aaaaaaaaa

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668

(2) INFORMATION ON SEQ ID NO. 86:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 671 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

ggaaaaccggt ctcatatgaac tcgcctgcag ctcttgggtt ttttgtggct tccttcgtta 60
tgggagccag gcctacacccc cagcaaccat gtccaaaggga cctgcagttt gtatttatctt120
tggcaccacc tactcttgtg tgggtgtttt ccagcacgga aaagtgcaga taattgccaai180
tgatcaggga aaccgaacca ctccaaagcta tgtcgccttt acggacactg aacggttcat240
cggtgatgcc gcaaagaatc aagttgcaat gaaccccacc aacacagttt ttgatgcca300
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aaaaaaagggt t 671

(2) INFORMATION ON SEQ ID NO. 88:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

agtggaggag ggagagacgc tggcccggga cccgaggggc gtgggcattcg ggaggcgggc 60
 ccgggttaagg ggcgggaccg ccgcctggtt aaaggcgctt atttcccagg cagccgctgc 120
 agtcgcccaca cctttcccccc tgctgcgatg accctgtcgc cacttctgct tcggacgtcc 180
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 cagttacta caagacaggc aatctataacc tgcgggggccc cctgaagaag tccaatgcac 300
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 agcttagcctt cctgaccatt gtctgcattgg aagagtttgaa ggacatggag agaagtctgc 600
 cactatgcct gcagctctac gccccaggcc tgcggccaga cactatcatg gagtgtgcaa 660
 tgggggaccg cggcatgcag ctcatgcaccc ccaacccccca ggggacagat gctctccagc 720
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 cccaaaaaaaaaaa aaaaccgcgt cggtcgac 1108

(2) INFORMATION ON SEQ ID NO. 89:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 720 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

aaagca~~gccc~~ ccggcgccgg gtgcctcaca gcacgctgcc acgcccacgc agacccctct 60
 ctgcacgc~~cc~~ gccc~~cccc~~gc acccaccatg gccacagtcc agcagctgga aggaagatgg 120
 cgcctgggg acagcaaagg ctttgatgaa tacatgaagg agcttaggagt gggaaatagct 180
 t~~tg~~cgaaaaa tggcgcaat ggccaagcc gattgtatca tcacttgc~~t~~ tgtaaaaac 240
 ctcaccataa aaactgagag cactttgaaa acaacacagt tttcttgc~~t~~ cctgggagag 300
 aagt~~ttt~~gaag aaaccacagc t~~g~~atggcaga aaaactcaga ctgtctgcaa ctttacagat 360
 ggtgcattgg tt~~c~~agcatca ggagtggat gggaaaggaaa gcacaataac aagaaaattg 420
 aaagatggg aatttagtggt ggagtgtgc atgaacaatg tcac~~c~~ctgtac tcggatctat 480
 gaaaaa~~g~~atg aataaaaatt ccatcatcac tttggacagg agttaat~~aa~~ gagaatgacc 540
 aagctcagtt caatgagcaa atctccatac t~~g~~tttcttc tttttttt cattactgtg 600
 ttcaattatc tt~~t~~atcataa acat~~tt~~taca tgcagctatt tcaaagtgtg ttggattaat 660
 taggatcatc cctttggta ataaataaat gtgtttgtgc taaaaaaaaaaaaaaaa 720

(2) INFORMATION ON SEQ ID NO. 90:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 837 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

ctctcg~~cg~~gag gattggctgt tagcggcg~~t~~ t~~g~~atgttaa~~g~~c tcgtgt~~a~~ac~~g~~ gccggcggtgt 60
 cggcag~~ct~~gc t~~g~~tagcgaag agagttggc g~~c~~gatgtctc acaccat~~ttt~~ gctgg~~t~~acag 120
 cctaccaaga ggccagaagg cagaacttat gctgactac~~g~~ aatctgtgaa tgaatgc~~t~~atg 180
 gaagg~~ttt~~gtt~~t~~ gtaaaatgt~~a~~ tgaagaacat ctgaaaagaa tgaatccaa cag~~t~~ccctct 240
 atcacat~~at~~g acatc~~at~~gtca gttgtt~~t~~at t~~t~~atc~~t~~gt~~c~~ atctggcaga c~~c~~tca~~g~~ctgc 300
 ctgg~~ttt~~acc gag~~c~~t~~g~~atac ccagacatac c~~a~~gc~~c~~tata acaaagactg gattaaagag 360
 aagat~~c~~tac~~g~~ t~~g~~tc~~c~~ttc~~g~~ tcggcaggcc caacaggctg ggaaataatt gtgttggaaag 420
 cactgggggg gttgggg~~t~~gg gcttggaaaca cagg~~t~~gt~~g~~t~~g~~ta c~~a~~gc~~t~~g~~c~~t~~g~~ tagtggaaag 480
 tttgtatcat agtaatc~~ct~~g tttccactt~~t~~ g~~t~~tatactct agccaaagatt gactgtat~~ta~~ 540
 gat~~g~~aaaatgt~~t~~ gaggat~~c~~t~~t~~g t~~t~~caatc~~g~~ga aacccccc~~g~~t ac~~c~~tcc~~c~~t~~t~~ tttttttctc 600
 tttttttt~~t~~ttttttact taaacat~~ttt~~ tatgatgatt tagatggaa~~g~~ ttgttcttc~~g~~ 660
 tcacttaat~~g~~ t~~g~~gg~~t~~cc~~g~~ t~~c~~ttcaact g~~t~~tcatatct actttataac attcacatac 720
 taacccttct~~t~~ tcaagatggg g~~t~~gggggg~~t~~g gaaatgc~~g~~t ttagccat~~g~~t cctcaagata 780
 aagtctt~~g~~gt aaaaataaat aaatgc~~c~~t~~t~~ tagttataaa aaaaaaaaaaaaaaaa 837

(2) INFORMATION ON SEQ ID NO. 91:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 498 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:
- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

gtagggtcaag cgccggaggc ggttagtgacg gtggcgtttc cttgaggaag agtgagggtt 60
ccaaacttttc tgcttatctg ggaggtgtg ggccggaca gtcgagatgt cagagaaaaa120
gcagccggta gacttaggtc tgtagagga agacgacgag tttgaagagt tccctggcgaa180
agactgggtt ggcttagatg aagatgaaga tgcacatgtc tggggaggata attgggatgaa240
tgacaatgtt gaggatgact tctctaatca gttacgagct gaactagaga aacatggta300
taagatggag acttcatacg atccagaaga agtgttgaag taacctaacc ttgacctgct360
taatacattc tagggcagag aacccaggat gggacactaa aaaaatgtgt ttatccatt420
atctgcttgg atttatttgtt gtttttgtaa cacaaaaat aaatgtttt atataaaaag480
gaaagagaaaa aatttgcgg 498

(2) INFORMATION ON SEQ ID NO. 92:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1077 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

cggttcggc tggataacaaca gggcacacgt gttcacgtt gacaggttg ctggggacgc 60
tagtaaccat gggcttgctg acttagccaa agaagagttt agaagaaaat acacacaagt 120
atacagactg ttcttagttt ctttagactt tctgcatttt ggataaaaata aatgcatttg 180
tgctttcat ttaggatgtt ttcatgttct ttaagatgtt ttaggaatgtt caacagagca 240
aggagaaaaa aggcaagtccct ggaatcacat tcttagcaca cctacacccctt ttggaaaatag 300
aacaacttgc agaatttggaa gtgattccctt tcctaaaatgt gtaagaaagc atagagattt 360
gttcgttattt agaatgggat cacgaggaaa agagaaggaa agtgattttt ttccacaaga 420
tctgtatgtt tatttccact tataaaggaa ataaaaaaatgt aaaaacatttt ttggatatc 480
aaaagcaat aaaaaccccaa ttcaagtctt tctaagcaaa attgctaaag agagatgaac 540
cacattttaa agtaatcttt ggctgttaagg cattttcatc ttcccttcgg ttggcaaaa 600
tatatttaaag gtaaaacatgtt ctgggtgaaacc aggggtgttg atggtgataa gggaggata 660
tagaatgaaa gactgaatctt ccctttgttgc cacaatataga ttggggaaa agcctgtgaa 720
aggtgtcttc tttagctttaa tgctttaaa agtatccaga gatactaca tattaacata 780
agaaaaagatt atatattttt tctgaatcga gatgtccata gtcaaaatttg taaaatcttt 840
tctttgttaa tattttatttt tattttatttt tgacagtggaa cattctgtattt ttaatgttaa 900
aacaagaaaaa gttgaagaag atatgtgaag aaaaatgtat ttttccttaaa tagaaataaa 960
tgatccccatt ttttggtaaa aaaaagatgtg tgagattttt tcgtaaacgt gactacttt 1020
tttctaaata agagattccc tacctgcgtc ctacaaggcag ttcagaatgc catgcct 1077

```

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1755 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

cgcaaggctg ctgtgatct ggtacgagga ttatgcaagt ttttgaggg acctgtgaca 60
 ggaatcttct ctggttatgt taattccatg ctgcaggaat acgcaaaaaa tccatctgtc 120
 aactggaaac acaaagatgc agccatctac ctatgtacat ctttggcatc aaaagccaa 180
 acacagaagc atggaattac acaagcaaata gaaacttgtaa acctaactga gtctttgtg 240
 aatcacatcc tccctgattt aaaatcagct aatgtgaatg aatttcctgt ccttaaagct 300
 gacggtaica aatatattat gatTTTtaga aatcaagtgc caaaagaaca tcttttagtc 360
 tcgattccctc tcttgattaa tcatctcaa gctgaaagta ttgttggta tacttacgca 420
 gctcatgctc ttgaacggct ctttactatg cgagggccta acaatgccac tctctttaca 480
 gctgcagaaa tgcaccggt tggtagatt ctgctaacaa acctttcaa agctctcaca 540
 cttcctggct cttcagaaaaa tgaatataattt atgaaagcta tcatgagaag tttttctc 600
 ctacaagaag ccataatccc ctatccctt actctcatc ctcagcttac acagaagct 660
 ttagctgtta taaagaataac ttgcaaagct aaccctgtctg ctgttggaaa ttttggaggag 720
 gctttttttt tgggttttac taaaatctta caaaatgatg tgcaagaatt tattccatac 840
 gtcttcaag tggatgtttt gcttctggaa acacacaaaaa atgacatccc gtcttccat 900
 atggccttat ttccctcatct cttcagcca gtgtttggg aaagaacagg aaatattcc 960
 gctctagtga ggcttcttca agcatttta gaacgcgggtt caaacacaat agcaagtgt 1020
 gcagctgaca aaattccctgg gttacttaggt gtcttcaga agctgattgc atccaaagca 1080
 aatgaccacc aaggttttt tcttctaaac agtataatag agcacatgcc tcctgaatca 1140
 gttgaccaat ataggaaaca aatcttcatt ctgttattcc agagacttca gaattccaa 1200
 acaaccaagt ttatcaagaaat ttttttagtc ttattttat tttttagtc ataaatatggg 1260
 gcactagcac tacaagaaaat attttaggtt atacaacaa aaatgtttgg aatgggtttg 1320
 gaaaaaattt ttattccctga aattcagaag gtatctggaa atgttagagaa aaagatctgt 1380
 gcggttggca taacccaaatt actaacagaa tggcccccaaa tgatggacac tgagtatacc 1440
 aaactgttggc ctccatttattt acgttcttgg attgggtttt ttgagttacc cgaagatgt 1500
 accattccctg atgaggaaca ttttatttgc atagaagata caccaggata tcagactgcc 1560
 ttctcacagt tggcatttgc tggaaaaaaa gagcatgatc ctgttaggtca aatgggtaa 1620
 aaccccaaaa ttcacctggc acagtcaattt cacaagttgtt ctaccgcctg tccaggaagg 1680
 gtccatcaa tggcaagaa ctctgtata aatggagact ttaatgggag ggcaaaaggaa 1740
 tagtagtagt tctgg 1755

(2) INFORMATION ON SEQ ID NO. 94:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

gttcgccgca~~g~~ cgagcacctt cgacgcggtc cggggacccc tcgtcgctgt cttccccacg 60
 cggacc~~cc~~cggt gccccaggct cgcgctgccc ggcaagggtgc tcgtgtc~~cc~~a ctccccggc~~g~~ 120
 acgc~~c~~ccccgg cgagtccccgg gccccctccc c~~t~~cgccgcgc gc~~c~~agatcg 180
 gccccccgc~~g~~ aggtcctcgc gttcg~~gg~~ctt ctgttgccg cggc~~g~~acggc gactttg~~cc~~ 240
 gca~~g~~ctcagg aagaatgtgt ctgtgaaaac tacaagctgg ccgtaaactg ctttgt~~ga~~at 300
 aataatcg~~c~~ aatgcc~~ag~~tg tacttcagg ggtgcacaaa atactgtcat ttgtc~~aa~~ag 360
 ctggctgcca aatgtttgg~~t~~ gatgaaggca gaaatgaatg gctcaaact tgggagaaga 420
 gcaaaac~~ct~~g aaggggccct ccagaacaa~~t~~ gatgggctt atgatc~~ct~~ga ctgc~~g~~atg~~ag~~ 480
 agcgggctct ttaaggccaa g~~c~~agtgc~~a~~ac gg~~c~~ac~~c~~tcca t~~g~~tgctgg~~t~~ t~~g~~tg~~a~~acact 540
 gctgggg~~t~~ca gaagaacaga caaggacact gaaataac~~ct~~ gctctgagcg agt~~g~~agaacc 600
 tactggatca tcattgaact aaaacacaaa gcaagagaaa aac~~c~~ttat~~g~~ta tagaaaa~~ag~~ 660
 ttgc~~gg~~actg cacttc~~ag~~aa gg~~g~~atc~~ac~~ a~~c~~cg~~gt~~tatc aactggatcc a~~a~~attt~~t~~atc 720
 ac~~g~~agtattt t~~g~~tat~~g~~agaa taatgtt~~t~~atc actattgatc t~~g~~gttcaaaa ttcttct~~ca~~ 780
 aaaactcaga atgatgt~~g~~ga cata~~g~~ct~~g~~at gt~~g~~ctt~~t~~attt atttt~~g~~aaaa agatgt~~ta~~aa 840
 ggt~~g~~aat~~c~~c~~t~~ t~~g~~ttt~~c~~attc taagaaaatg gac~~c~~t~~g~~acag taaatggg~~g~~ acaactggat 900
 ctggat~~c~~ctg g~~t~~caaactt~~t~~ aatttat~~t~~at~~t~~ g~~t~~at~~g~~aaa a~~g~~cac~~c~~t~~g~~a attctcaat~~g~~ 960
 cagg~~g~~ctaa aagctgg~~t~~g~~t~~ tatt~~t~~ctg~~t~~ttt~~t~~at~~t~~ g~~t~~gt~~g~~at~~g~~c agt~~t~~gtt~~g~~ct~~l~~020
 ggaattt~~g~~tg~~t~~ t~~g~~t~~g~~ttat~~t~~ttccagaaa aagagaat~~g~~ gaa~~g~~at~~g~~ta g~~a~~agg~~g~~t~~g~~ag~~l~~080
 ataaaaggaga t~~g~~gg~~g~~gagat~~t~~ g~~c~~atagg~~g~~aa c~~t~~caat~~g~~cat aactatataa t~~t~~tg~~a~~agat~~l~~140
 atagaagaag g~~g~~aaat~~g~~ag~~ca~~ aatggacaca aattacaaa~~t~~ g~~t~~gt~~g~~tc~~g~~t g~~g~~gac~~g~~a~~g~~al1200
 catctt~~g~~aa g~~g~~t~~c~~at~~g~~at~~t~~tt~~t~~tt~~t~~ aacat~~c~~at~~t~~ a~~t~~tt~~t~~g~~t~~ata~~t~~ g~~t~~g~~a~~aa~~c~~ct~~g~~~~l~~260
 tact~~ca~~aa~~t~~at~~g~~c~~g~~t~~t~~ t~~g~~aaact~~g~~gc t~~t~~acc~~a~~at~~c~~ t~~t~~g~~a~~aa~~t~~tt~~g~~ accaca~~a~~gt~~g~~~~l~~320
 t~~c~~t~~t~~at~~at~~at~~t~~ g~~c~~ag~~at~~c~~ta~~ t~~g~~aaaat~~cc~~ a~~g~~aact~~tt~~g~~g~~a c~~t~~ccat~~cg~~tt a~~aa~~attt~~at~~tt~~l~~380
 at~~g~~t~~g~~taaca t~~t~~caa~~at~~gt~~g~~ t~~g~~c~~at~~aaa~~t~~ at~~g~~ctt~~cc~~ac agt~~aa~~at~~ct~~ g~~aaa~~act~~g~~al1440
 t~~t~~tt~~g~~gatt~~t~~ aaagctgc~~c~~ t~~t~~c~~t~~attt~~t~~ac~~t~~ t~~t~~g~~ag~~t~~c~~tt~~t~~ tacata~~c~~ata~~t~~ c~~t~~tttttat~~g~~l1500
 agctat~~g~~aaa taaaac~~at~~tt~~t~~aaaact~~g~~aaa aaaaaaaaaa aaggc 1545

(2) INFORMATION ON SEQ ID NO. 95:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ggcgggtatt atcgggtaga catctcgac cgccgttcgg aaaccggtag cgcttcgcgc 60
 atggctgacc aactgactga agagcagatt gcagaattca aagaagctt ttcactattt 120
 gacaaaatgt gtatggaaac tataacaaca aaggaaattgg gaactgtaat gagatcttt 180
 gggcagaatc ccacagaagc agagttacag gacatgatta atgaagttaga tgctgttgt 240
 aatggcacaa ttgaacttcc ctgaatttct ggacaaggat ggcaagaaaa atgaaagaca 300
 cagacagtga agaagaaaatg agagaagcat tccgtgttt tgataaggat ggcaagggt 360
 atatgagtgc tgcagaacctt cgccatgtga tgacaaacctt tggagagaag ttaacagatg 420
 aagaagtgtga tgaaatgatc agggaagcag atattgtatgg tgatggtcaa gtaaactatg 480
 aagagtgtgt acaaatgtatc acagcaaagt gaagacctt tacagaatgt gttaaatttc 540
 ttgtacaaaaa ttgttttattt gccttttctt tggtttaac ttatctgtaa aaggtttctt 600
 cctactgtca aaaaaatatg catgtatagt aattaggact tcattccctcc atgttttctt 660
 cccttatctt actgtcattt tcctaaaaacc ttatTTTttaga aaagttgatc aaggtaacat 720
 gttgcatgtg gcttactctg gggaaatatc taagcccttc tgccatcta aacttagatg 780
 gagttggtca aatgaggaa catctgggtt atgccttttt taaagttagtt ttcttttagga 840
 actgtcagca tgggttttttggtaa gaaatgtgttttggtaactc tgctggact atggacagtc 900
 aacaatatgt acttaaaatgt tgcaactatttgc caaaacgggt gtattatcca ggtactcgta 960
 cactattttt ttgtactgtt ggtcctgtac cagaaacatt ttcttttattt gttacttgct 1020
 ttttaaactt ggttagcca cttaaaatct gcttatggca caatttggcc caaaatccat 1080
 tccaagttgtt atattttttt tccaaataaaa aaattacaat ttacccaaaaaaa 1133

(2) INFORMATION ON SEQ ID NO. 96:

- (i) SEQUENCE CHARACTERISTIC:**
 - (A) LENGTH: 791 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:** partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL:** NO
- (iv) ANTI-SENSE:** NO
- (vi) ORIGIN:**
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:**
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

ggccggcccg  cgagccccggc  gagaggccg  ggcggggagcg  gcgggtatgg  acgggtccgg  60
ggagcagccc  agagggcgggg  ggccccaccag  ctctgagcag  atcatgaaga  cagggggccct 120
tttgccttcag  ggtttcatcc  aggatcgagc  agggcgaatg  ggggggggagg  caccggagct 180
ggccctggac  ccggtgccctc  aggatcgctc  caccaagaag  ctgagcgaqt  gtctcaagcg 240
catcggggac  gaactggaca  gtaacatgga  gctgcagagg  atgattccg  ccgtggacac 300
agactcccccc  cgagagggtct  tttcccgagt  ggcagctgac  atgtttctg  acggcaactt 360
caactggggc  cgggttgtcg  ccctttcta  ctttgcgcagc  aaactggtgc  tcaaggccct 420
gtgcaccaaag  gtgccggaaac  tgatcagaac  catcatgggc  tggacattgg  acttcctccg 480
ggagcggtctg  ttgggtgtgg  tccaagacca  ggggtgggtgg  gacggcctcc  tctctactt 540
ttggacgccc  acgtggcaga  ccgtgaccat  ctttgggtggc  ggagtgccta  ccgcctcact 600
caccatctgg  aagaagatgg  gctgagggcc  ccagctgcct  tggactgtgt  ttttcctcca 660
taaattatgg  cattttctg  ggaggggtgg  ggatgggggg  acatggcat  ttttcttact 720
tttgttaatta  ttgggggggtg  tggggaaagag  tggtgtttag  ggggtataaa  acctccctcg 780
ggacacaaaaa  a

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791

(2) INFORMATION ON SEQ ID NO. 97:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 599 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

tcctgccttc accatgaagt ccagcggcct cttcccccttc ctgggtgtgc ttgcccctggg 60
aactctggca ccttgggctg tggaaggctc tgaaaagtcc ttcaaaagtctg gagtctgtcc 120

tcctaaaaaa tcgtccccagt gccttagata caagaaaacct gagtgccaga gtgactggca 180
gtgtccaggg aagaagagat gttgtctctga cacttgtggc atcaaattgtcc tgatgtctgt 240
tgcacacccca aaccccaacaa ggaggaagcc tggaaagtgc ccagtgtactt atggccaaatg 300
tttgtatgtttt aaccccccacca atttctgtgtga gatggatggc cagtgtcaaggc gtgactttgaa 360
gtgttgtcatg ggcatgtgtgtggaaatctgtcgatggatggc cagtgtcaaggc gtgactttgaa 420
atatggagga ggctctggas tcctgtctgtgtggatggcag gtcccttccca ccctgagact 480
tggctccacc actgatatatcc tcctttgggg aaaggcttgg cacacagcag gctttcaaga 540
agtgtccatgtt gatcaatgaa taaaataaaacgtggatatttc tctttgtcaaa aaaaaaaaaa 599

(2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 643 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ggggcccgccg ctcgggcgt a ggaggcggtg cctctgcagc a a g c g t g g g g c g c g g g a a c c 60
 cgacgaggac tctccagtcc tcagtcacct tggacaaaga agtgtggatc ctca gattcc 120
 atctttcca actccaaggt gccatggcag agaagggtgct ggtAACAGGT gggctggct 180
 acattggcag ccacacggtg ctggagctgc tggaggctgg ctacttgcc tgggtcatcg 240
 ataacttcca taatgccttc cgtggagggg gctccctgcc tgagagcctg cggcgggtcc 300
 aggagctgac aggccgctct gtggagttt aggagatgga catttggac caggagcccc 360
 tacagcgctc cttcaaaaag tacagctta tggccgtcat ccactttgcg gggctcaagg 420
 ccgtggcga gtcggcgtcag aagcccttgg attattacag agttaacctg accgggacca 480
 tccagcttggagatcatg aaggccccacg gggtaagaa cctggtgttc a g c a g t c a g 540
 ccactgtgt a cggaaacccc c agtacctgc ccccttgaat gagggccacc ccacgggtg 600
 ggatgtaaaca accttacgga agtccaaatt tcttatctt ttc 643

(2) INFORMATION ON SEQ ID NO. 99:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 860 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

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ctcgagccgc tcgagccgat tcggctcgag tgccctccaga ggactggcca cattttgcct 60
agataaaagat gcacttagag atgaatatga tgcatttcata gatgttgaatg cagtgacaaat120
ggagagtgtt cgagaatggg aaatgcagtt taaaagaaaaa tatgattatg taggcagact180
cttaaaacca ggagaagaac catcagaata tacagatgaa gaagatacca aggatcacaa240
taaacaggat tgaactttgt aaacaaccaa agtcaggggc ctgcagaact gcaattctta300
ctcccttca cagactgtcc ggagtcttgc ggtttgattc acctgctgcg aaaaacattc360
aacaaaattgt gtacaagata attaatctc actatgaaaga tttgaataac tagacattat420
ttatgctgcc aaactcattt gttgcagttt ttgttaatgt ctatgtgggc ttcatcatcc480
tggaaaagaag gagacagggg tttttttaaa gagaagaaa gtcacaatata tacttctttc540
cttcctttt tcccttcttc ctttcttctt tctctttctt tctttttaaa atatattgaa600
gacaaccaga tatgtatttt ctactcaagt gtacagatct cctcaagaaa catcaaggaa660
ctcctgtgtc acatactgtg tttttatttt aacatgggtg agggaggcga cctgatcagg720
ggaggtgggg gtacacatca atttgagttt ttcaggctac taaaacatta aaatgtgaat780
tcccaaactt ttcttttgg cattgttcgg gggataggga aatatcgaaa taaaaggagt840
cttggaaatt ggtgtggaa 860
```

(2) INFORMATION ON SEQ ID NO. 100:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

ccggggctccgc ccagcctgggt ccggggagag qactggctgg gcaggggcgc ccccccccct 60
 cgggagacgc gggccggggcg gggctggag tattttaggc tcggagccac cgccccggcg 120
 gccccccgcag caccctcccg ccagcagccg tccggagcca gccaacgagc ggaaaatggc 180
 agacaattt tcgtccatg atgcgttatac tgggtctgg aacccaaacc ctaaggatg 240
 gctggcgca tgggggaacc agcctgtgg ggcaggggc taccagggg ctccctatcc 300
 tggggctac cccggcaagg caccccaagg ggcttatact ggacaggcac ctccaggcgc 360
 ctaccctggc acacccctggag ttatcccg agcacctgca cctggagtct acccaggccc 420
 acccagccgc cctggggctt acccatcttc tggacagcca agtgccaccc gagcttaccc 480
 tgccactggc ccctatggcg ccctgtgtt gcaactgatt gtgccttata acctgcctt 540
 gctggggga gtggtgccct gcatgtgtat aacaattctg ggcacgggtga agccaaatgc 600
 aaacagaatt gcttttagatt tccaaagagg gaatgtatgtt gccttccact ttaacccacg 660
 cttcaatcgag aacaacagga gacttattgt ttgtcaataca aagctggata ataactgggg 720
 aagggaagaa aacagtcgg tttccatt tggaaagtggg aaaccatca aaatacaatgt 780
 actgggttga cctgaccact tcaaggttgc agtgaatgtat gtcacttgt tgcaagtacaa 840
 tcattgggtt aaaaaactca atgaaatcag caaactggga atttctgtg acatagacct 900
 taccagtgt tcatataccat tgatataatc tggaaaggccc agattaaaaa aaaaaaaaaa 960
 atctaaacct tacatgtgtt aagggttcat gttcaactgtg agtggaaatt tttacattca 1020
 tcaatatccc tcttgttaagt catctactta ataaatatta cagtggaaaa aaaaaaaaaa 1080
 aaaaaaaaaa gtggaaaaag gaggggggaaag gagagagagg gaagaagaga gagggagaagg 1140
 aggggggggggg tgggt 1155

(2) INFORMATION ON SEQ ID NO. 101:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 522 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

aaaaatattt gctggaaatt gctgtgttagg attacaggcg tgaccactgc gcccggccac 60
 attcagttct tatcaaagaa ataacccaga cttaatctt aatgatacga ttatgccca 120
 tattaagtaa aaaatataag aaaaggttat cttaaataga tcttagggcaa aataccagct 180
 gatgaaggca tctgatgcct tcattgttgc agtcatctcc aaaaacagta aaaataacca 240
 ctttttgttggcaatatga aatttttaaa ggatggaaat accaaatgtat agaaacagac 300
 tgcctgaatt gagaatttttgc atttctttaa gtgtgtttct ttctaaatttgc tgcattttta 360

atttgattaa tttaattcat gtattatgtat taaatctgag gcagatgagc ttacaagtat420
 taaaataatt actaattaat cacaatgtg aagttagtgc tgatgtaaaa aataacaaaca480
 ttcttaattaa aggctttgca acacaaaaaa aaaaaaaaaa aa 522

(2) INFORMATION ON SEQ ID NO. 102:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

ccagctcgcc ctgcctagcc aggggcgccc cgccccctgc ctgcccggcc acttcggga 60
 gcccgttcca ataggcggtc gccattggct ctggcgacct ccgcgcgttg ggaggtgttag 120
 cgcggctctg aacgcgctga gggccgttgta gtgtcgcaagg cggcgagggc gcgagtgagg 180
 agcagaccca ggcacatcgcc gcccagaagg cccggcgctcc ccacactgaa ggtccggaaa 240
 ggcgacttcc gggggcttgc gcacctggcg gacccctcccg gagcgtcggc acctgaacgc 300
 gagggcgctcc attgcgcgtg cgcggttgggg ggcttcggc acctgtatgc gagaccccaa 360
 cggctggtgg cgtcgccctgc gcgtctcgcc tgatgtggcc atggcgcagt gtgcgggctg 420
 aggccggagcg ggcgtttctc gcccctgtgg gatcgctgtct cctctctgggg gtcttggcg 480
 ccgaccgaga acgcagcatc cacgacttct gcctgggtgtc gaagggtggg ggcagatgcc 540
 gggcctccat gccttaggtgg tggtaaatgc tcactgacgg atccctggcag ctgtttgtgt 600
 atgggggctg tgacggaaac agcaataatt acctgaccaa ggaggagtgc ctcaagaaat 660
 gtgccactgt cacagagaat gccacgggtg acctggccac cagcagaaat gcagcggatt 720
 cctctgtccc aagtgtccc agaaggcagg attctgaaga ccactccagc gataatgttca 780
 actatgaaga atactgcacc gccaacgcag tcactggcc ttggcgatgc tccttcccac 840
 gctggtaactt tgacgtggag aggaacttgc gcaataactt catctatggg ggctgcccggg 900
 gcaataagaa cagctaccgc tctgaggagg cctgcatgtct ccgctgttcc cgccagcagg 960
 agaattccccc cctgccccctt ggctcaaagg tggtggttct ggccggggctg ttctgtatgg 1020
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 aggagcgtgc cctgcgcacc gtctggagct ccggagatga caaggagcag ctgtgaagall 1140
 acacatatgt cctgtgaccg ccctgtcgcc aagaggactg gggaaaggag gggagactat 1200
 gtgtgagctt tttttaaaata gagggttga ctcggatttg agtgcatttggggctgagg 1260
 tctgtttctc tggaggtag gacggctgtct tcttgggtctg gcaggatgg gtttgcgtt 1320
 gaaatccctt aggaggctcc tcctgcatg gcctgcagtc tggcagcagc ccccgatgt 1380
 ttccctcgctg atcgatttct ttccctccagg tagagtttc tttgcttatg ttgaattcc 1440
 ttgcctctt tctcatcaca gaagtgtatgt tgaatcggtt tctttgttt gtctgat 1500
 tggttttttt aagtataaac aaaagttttt tattagcatt ctgaaagaag gaaagtaaaa 1560
 tgtacaagtt taataaaaaag gggcctcccc cttagaata aaaaaaaaaa 1620
 aaaaaaaaaa 1628

(2) INFORMATION ON SEQ ID NO. 103:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 605 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

cctggcagct gtcggctgga aggaacttgt ctgctcacac ttgctggctt gcgcattcagg 60
actggctta tctccgtact cacggtgcaa aggtgcactc tgcaacgtt aagtccgtcc 120
ccagcgcttg gaatcctacg gccccccacag ccggatcccc tcagccttcc aggtcctca 180
ctccccggaa cgctgaacaa tggcctccat gggctacag gtaatggca tcgcgctggc 240
cgtcctgggc tggctggccg tcatgctgtg ctgcgcgctg cccatgtggc gcgtgacggc 300
cttcatcgcc agcaacattg tcacctcgca gaccatctgg gagggcttat ggatgaactg 360
cgtggtgccag agcaccggcc agatgcagtg caaggtgtac gactcgctgc tggactgcc 420
gcaggacctg caggcgcccc gcgcctcgat catcatcagc atcatcggtt ctgctctggg 480
cgtgctgctg tccgtggtgg ggggcgaagt gtaacaaact tgcctggagg attaaaagcg 540
ccaaggcaca gaacatgatt cgttggcggg cgtgggttt tctgtttggg ccggcctaatt 600
gggtg 605

(2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 2731 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

agggggggcgg acagacacag actatgcaga tgggagtgaa gacaaagttag tagaagttagc 60
 aqaggaggaa gaagtggctg aggtggagga cgatgaggat ggtgatgagg tagaggaaga 120
 ggctgaggaa ccctacgaag aagccacaga gagacacaga gtctgtggaa gaggtggttc 180
 gagaggtgtg ctctgaacaa gcccagacgg ggcctgtcccg agcaatgatc tcccgctggt 240
 actttgtatgt gactgaaggg aagtgtgccc cattttta cggcggatgt ggcggcaacc 300
 ggaacaactt tgacacagaa qagtaactgca tggccgtgtg tggcagcgc attctacaaa 360
 cagcagccag taccctgtat gccgttgaca agtatctcgaa gacacctggg gatgagaatg 420
 aacatgccca ttccagaaaa gccaaagaga ggcttgaggc caagcaccga gagagaatgt 480
 cccaggtcat gagagaatgg gaagaggcag aacgtcaagc aaagaacttg cctaaagctg 540
 ataagaaggc agttatccag catttccagg agaaaagtggaa atctttggaa caggaagcag 600
 ccaacgagag acagcagctg gtggagacac acatggccag aqgttggaaagcc atgtcaatg 660
 accgcccggc cctggccctg gagaactaca tcaccgtct gcaggctgtt cctctcgcc 720
 ctctgtcacgt gttcaatatg ctaaaaagaatg atgtccgcgc agaacacaaag gacagacagc 780
 acaccctaaa gcatttcgag catgtgcgc tgggtggatcc caagaaagcc gctcagatcc 840
 ggtccccaggt tatgacacac cttccgtgtgat tttatgagcg catgaatcag tctctctccc 900
 tgctctacaa cgtgcctgtca gtggccgagg agattcagga tgaagttgtat gagctgcttc 960
 agaaagagca aaactattca gatgacgtct tggccaacat gattagtgaa ccaaggatcal020
 gttacggaaa cgatgctctc atgccatctt tgaccgaaac gaaaaccacc gtggagctcc1080
 ttcccgtgaa tggagagttt acgcttggacg atctccagcc gtggcatttttggggctgl140
 actctgtgcc agccaacaca gaaaacaaag ttgacccctgt tgatgcccgc cctgctgccc1200
 accggagact gaccactcgccaggttctg gtttgcacaaa tatcaagacg gaggagatctl1260
 ctgaagtggaa gatggatgtca gaaattccgac atgactcagg atatgaatgat catcatcaa1320
 aatttgggtt ctttgcagaa gatgtgggtt caaacaaaagg tcaaatcatt ggactcatgg1380
 tgggcgtgt tgcatacgac acagtgtatcg tcatacacctt ggtgatgtg aagaagaaac1440
 agtacacatc cattcatcat ggtgtgggg aggttgcgc cgctgtcacc ccagaggagc1500
 gccacctgtc caagatgcag cagaacggct acgaaaatcc aacctacaag ttcttgagc1560
 agatgcagaa cttagcccccc gccacacgcg cctctgaagt tggacagacaa aaccattgct1620
 tcactaccca tcgggtgtcca tttatagaat aatgtggaa gaaacaaacc cgtttatgal680
 tttactcatt atgcctttt gacagctgtg ctgttaacaca agtagatgcc tgaacttgaal740
 ttaatccaca catcagtaat gtattctatc tctcttaca ttttggtctc tataactacat1800
 tattaatggg ttttgttac tggtaaagaat ttagctgtat caaaacttagt catgaatagal860
 ttctctccctg attatattatc acatagcccc tttagccagtt gtatattatt cttgtggttl1920
 gtgacccaat taagtccctac tttacatatg cttaagaat cgatggggga tgcttcatgtl1980
 gaacgtggga gttcagctgc ttctcttgc taagtattcc tttcctgtatc actatgcatt2040
 ttaaaagttaa acattttaa gtattcaga tgcttttagag agatgtttt tccatgactg2100
 cattttactg tacagattgc tgcttctgtat atattgtga tataggaatt aagaggatac2160
 acacgtttgt ttcttcgtgc ctgtttttagt tgccacacatt aggcatggag acttcaagct2220
 tttttttttt tggccacgtt cttttgggtc tttgataaaag aaaagaatcc ctgttcattg2280
 taagcacttt tacggggcgg gtggggaggg gtgtctgtct ggtcttcaat taccagaat2340
 tctccaaaac aattttctgc aggatgattg tacagaatca ttgctttaga catgatcgct2400
 ttctacactg tattacataa ataaattaaa taaaataacc cccggcaaga cttttctttg2460
 aaggatgact acagacatta aataatcgaa gtaattttgg gtggggagaa gaggcagatt2520
 caatttctt taaccagtct gaagtttcat ttatgataca aaagaagatg aaaatgaaag2580
 tggcaatata aggggatgag gaaggcatgc ctggacaaac ctttctttta agatgtgtct2640
 tcaatttgta taaaatggtg ttttcatgtta aataaataca ttcttgagg agccaaaaaa2700
 aactatatta ctggcagggtt tataatatgg c

(2) INFORMATION ON SEQ ID NO. 106:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2194 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

gaattcagaa	gttaatgatg	ttgggtaaga	gaacaatgg	aagagagcaa	tctaagaata	60
tatcacctac	tttaatttta	tatgagagta	catggaggta	gctgtatgt	ggaaatgtag	120
cactgctcc	accacgcag	atttatttca	gtaaaacaac	aactggaact	tcaagtaact	180
cctccccagag	tacttccaac	tctgggttgg	ccccaaatcc	aactaatgcc	accaccaagg	240
cggtctgggg	tgccctgcag	tcaacagcca	gtctttcg	ggtctca	tcttttcgc	300
atctctactc	ttaagagact	caggccaa	aacgtttct	aaatttcccc	atcttctaaa	360
cccaatccaa	atggcgtctg	gaagtccaa	gtggcaagga	aaaacaggtc	ttcatcgaat	420
ctactaattc	cacacccccc	attgacacag	aaaatgttga	gaatccaaa	tttattgtat	480
tttgaagaaca	tgtgagaggt	ttgacttagat	gatggatgcc	aatattaaat	ctgtggagt	540
ttcatgttaca	agatgaagga	gaggcaacat	ccaaaatagt	taagacatga	tttcttggaa	600
tgtggcttga	gaaatatgg	cacttaatac	tacccctgaaa	ataagaatag	aaataaagg	660
ttggatttgt	gaatggagat	tcagtttca	tttgggtcat	taattctata	aggccataaa	720
acaggtaata	taaaaagctt	ccatgat	atttatatgt	acatgagaag	gaacttccag	780
gtgttactgt	aattcctcaa	cgtattttt	cgacagca	aatttaatgc	cgatataactc	840
tagatgaagt	tttacattgt	tgagcttatt	ctgttctt	gggaactgaa	ctcaacttcc	900
tcctgaggct	ttggatttga	cattgcattt	gaccctttat	gttagtaattt	acatgtgcca	960
gggcaatgt	gaatgagaat	ctacccccc	atccaagcat	cctgagaac	tcttattat	1020
ccatatttgg	tcaaatggta	ggcattttct	atcacctgtt	tccattcaac	aagagcaact	1080
cattcatta	gctaaacgg	ttccaaagag	tagaatttgc	ttgaccgcga	ctaatttcaal	1140
aatgctttt	atttatttta	tttttttagac	agttctactt	tgtccccag	gcccggagtgc	1200
agtggtgcg	tctcagatca	gtgttaccatt	tgcctcccg	gctcaagcg	ttctcctgccl	1260
tcagcctccc	aagttagctgg	gattacagge	acctgcccacc	atgcccggct	aattttgtat	1320
attttagtag	agacagggtt	tcaccatgtt	gcccaggctg	gtttcgaact	cctgacactcal	1380
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tgtatctgtt	tgaaggcaaa	atttgcataatc	ttgaaaattaa	gaaggcaaaa	atgtaaaggal	1560
gtcaaaaacta	taaatcaagt	atttgggaa	tgaagactgg	aagctaattt	gcattaaattl	1620
cacaaaactt	tatactt	ctgtatatac	attttttttc	tttaaaaaaaac	aactatggat	1680
cagaataagcc	acattttagaa	cacttttgt	tatcagtccaa	tattttttaga	tagttagaac	1740
ctggtcctaa	gcctaaaagt	gggtttgatt	ctgcagtaaa	tcttttacaa	ctgcctcgac	1800
acacataaac	ctttttaaaa	atagacactc	cccgaaagtct	tttggtcgca	tggtcacacal	1860
ctgatgctt	gatgttccag	taatctaata	tggccacagt	agtctttagt	accaaaagtcc	1920
tttttttcca	tcttttagaaa	actacatgg	aacaaacaga	tgcacacgtt	ttgaagctac	1980
tgtgtgtgt	aatgaacact	cttgctttat	tccagaatgc	tgtacatcta	tttggattg	2040
tatattgtgt	ttgtgttattt	acgcttgc	tcatagtaac	ttctttagga	attgatttgc	2100
attgaacaca	aactgttaat	aaaaagaaat	ggctgaaaga	gcaaaaaaaaa	aggaaagaaa	2160
aaagaaaaaa	aaaagaaaaaa	aaaaaggggg	aggc			2194

(2) INFORMATION ON SEQ ID NO. 107:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

cggaagggtgg accttggatg aattttgacg agaacaagtt cgtggaccga agaagatggg 60
ggccgcacgc ccaggcccgg gccccgacga ggcccggatg gacacctgcc ccctgcgc当地 120
aggaaacatg aaacagaccc tacaggcagc tctgaagaac cccccctatca acacccaagag 180
tcaggcagtg aaggaccggg caggcagcat tgtcttgaag gtgctcatct cttaaaagc 240
taatgatata gaaaaggcag ttcaatctct ggacaagaat ggtgtggatc tcctaataatgaa 300
gtatattttt aaaggatttg agagcccgatc tgacaatagc agtgctatgt tactgcaatg 360
gcatgaaaag gcacttgctg ctggaggagt agggtccatt gttcgtgtct tgactgcaag 420
aaaaactgtg tagtctggca ggaagtggat tatctgcctc gggagtggga attgctggta 480
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tggaaaattgg gataatatacg aagaaattgt gttaaaatag aagtgtttca tcctttcaaa 660
accatttcag tgatgtttat accaatctgt atataatgtata atttacattc aagttaattt 720
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actaataactg agagatttgg tcagaatattt agggcgtttt cctagctcat tgtagtcag 840
gaaatgatata ttataaaaaaa tatgagagac tggcagctat taacattgca aaactggacc 900
atattttccct tatttaataaa gcaaaatatg ttttttggat aagtgggg tgaataccac 960
tgccaagttt tagctttgtt tttgcttgcc tcctgattat ctgtactgtg ggttttaagtat 1020
tgctactttc tctcagcatc caataatcat gcccctcaa tttattttgt gtcacccagg 1080
gttcagagca agaagtcttg ctttatacaa atgtatccat aaaatatcag agcttgg 1140
gcatgaaacat caaacttttgc ttccactaat atggctctgt ttggaaaaaaa ctgcaaatca 1200
gaaagaatgaa ttgcagaaaa gaaagaaaaaa ctatgggtgtat atttaaactc tggcagcct 1260
ctgaatgaaa tgcactttc tttagaaata taatagctgc ctttagacatt atgaggatata 1320
caacttagtat ttaagatacc atttaatatg ccccgtaaat gtcttcagtg ttcttcagg 1380
tagttggat ctcaaaaagat ttggttcaga tccaaacaaa tacacattct gtgttttagc 1440
tcagtgtttt cttaaaaaaaag aaactgccac acagcaaaaa attgtttact ttgttggac 1500
aaccacaaatca gttctcaaaa aatgaccgggt gcttataaaa agttataaaat atcgagtagc 1560
tctaaaaacaa accacctgac caagaggaa gtgagcttgc gcttagtatt tacattggat 1620
gccagttttg taatcactga cttatgtgc aactggtgca gaaattctat aaactcttgc 1680
ctgtttttgtt tacctgtttt ttgtttcatt ttgtttttgtt ttgtaaaaat gataaaaactt 1740
cagaaaaataa aatgtcagtg ttgaataaaa taaaaaaaca aattgaagaa gaggatggag 1800
atttcgactt gg 1812

```

(2) INFORMATION ON SEQ ID NO. 108:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 890 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (v) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vi) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

aacgactcct ggtacacctgc tcccattact tcccgttttc tcgatctgct gctcgctca 60
ggctcgtagt tcgccttcaa catgccgaa ccagcgaagt ccgctccgcg gcccaagaag120
ggctcgaaaga aagccgtgac taaggcgac aagaaggacg gcaagaagcg caaggcagcc180
gcaaggagag ctactccgtta tacgtgtaca aggtgctgaa gcaggtccac cccgacaccg240
gcatactccctc taaggccatg ggaatcatga actccctcgta caacgcacatc ttgcAACGCA300
tcgcgggtga ggcttcccgc ctggcgccatt acaacaaggcg ctcgaccatc acctccaggg360
agatccagac ggccgtgcgc ctgctgctgc cccggggagtt ggccaaggcac gccgtgtccg420
agggcaccaa ggccgtcacc aagtacacca gcgctaagta aacttgccaa ggagggactt480
tctctgaaat ttccctgatat gaccaagaaa gcttcttataaaaagaagca caattgcctt540
cggttacctc attatctact gcaaaaaaga agacgagaat gcaaccatac ctagatggac600
ttttccacaa gctaaagctg gcctcttgat ctcattcaga ttccaaagag aatcatttac660
aagttatctt ctgtctccctt ggtccattcc ttctctctaa taatcattta ctgttcctca720
aagaattgtc tacattaccc atctccctt ttgcctctga gaaagaggtat ataagcttct780
gtaccccaact ggggggttgg ggtaatattc tgggtccctc agccctgtac cttaataaaat840
ttgtatgcct ttctcttaa aaaaaaaaaa aagaagaagg aagaggatgc 890

```

(2) INFORMATION ON SEQ ID NO. 110:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2627 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vi) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

(2) INFORMATION ON SEQ ID NO. 111:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 976 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

ctcgagccgc gagattcccc cgaaggctc catgaagcgc ctcaccggc gcctcatcgc 60
cgtcatcggt gtggtcgtgg tggccctcgt cgccggcatg gccgtctgg ttagtaccaaa120
ccggagaaaag tcggggaaagt acaagaaggt ggagatcaag gaactggggg agttgagaaa180
ggaacccggc ttgttaggtac ccggccgggc agggatggg gtggggtaacc ggatttcggt240
atcgcccccg acccaagtga gtcacgcctc ctgattccctc ggcgcaaaagg agacgtttat300
cctttcaaat tccctgccttc cccctccctt ttgcgcacac accaggtta atagatcctg360
gcctcagggt ctcccttctc ttcacttct gtcttgaagg aagcatttct aaaatgtatc420
cccttcgggt ccaacaacaag gaaacctgac tggggcagtg aaggaaggga tggcatagcg480
ttatgtgtaa aaaacaagta tctgtatgac aacccgggat cgtttgcacaa taactgaatc540
cattgcaca ttgtgaaggc ttaaatgagt ttatgtgggaa aatagcggtt ttatcgccctt600
gggtttaaat tatttgatga gttccacttg tatcatggcc tacccgagggaa gaagaggagt660
ttgttaactg ggcctatgta gtagcctcat ttaccatcggt ttgttattact gaccacatata720
gcttgtcaact gggaaagaag cctgtttcag ctgcctgaac gcagttggta tgtcttgag780
gacagacatt gcccggaaac tcagtttatt tattcttcag cttgcctta ctgccactga840
tattggtaat gttctttttt gtaaaatgtt tgtagatatg ttgtcttga taatgttgct900
gtaatttttt aaaataaaac acgaattttaa taaaatatgg gaaaggcaca caaaaaaaaa960
aaaaaaaaaaaaaaa aaaaaac

```

976

(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1427 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

cttccgggggt gactgcctct tccagggcgg gcggtgtgg gcacgcattg ctgtgctcca 60
actccctcag ggcctgtgtt gcccactct gctgctatga gcttcctcaa aagtttcccc 120
ccgctgggc cagcggaggg gctccctgcgg cagcagccag acactgaggc tgtgcigaac 180
ggaaagggcc tcggcactgg taccctttac atcgctgaga gccgcctgtc ttggtagat 240
ggctctggat taggattctc acttggataac cccaccatta gtttacatgc attatccagg 300
gaccgaagtg actgtcttagg agagcatttg tatgttatgg tgaatgc当地 atttgaagaa 360
gaatcaaaaag aacctgttgc tgatgaagaa gaggaagaca gtgatgtatg tggtaacct 420
attactgaat ttagatttgt gcctagtatg aatcagcgt tggaggcaat gttcaactgca 480
atgtgcgaat gccaggcctt gcatccagat cctgaggatg aggattcaga tgactacat 540
ggagaagaat atgatgtgga agcacatgaa caaggacagg gggacatccc tacattttac 600
acctatgaag aaggattatc ccatactaaca gcagaaggcc aagccacact ggagagatta 660
gaaggaatgc ttctcagtc tgtgagcagc cagtataata tggctgggt caggacagaa 720
gattcaataa gagattatga agatggatg gaggtggata ccacaccaac agttgctgga 780
cagtttggg atgcagatgt tgatcactga aaatgatita tgcaagttt agattctgct 840
cctaagtgtt ggagagaact tgggcctct tccactctgg agtgaagttt atgaaagtct 900
ttttcccttt caaaaaccca acctgaacca gttctttttt gagacagact atactgagac 960
aacaagttgt caccagcaga agatagataa tatgacccctt attaacttga tgaattaact 1020
taaccaagag ggtatgttta gtttactatt taccctaaaa ctttctgtgt ctgggtaccc 1080
tctgagtagg cctataattt ctaccttgac tggatgtgc当地 atttgtttaagc tagcagatct 1140
atgtggtaa aatgcacagg agcttggtag actgcggggg aaagagagag ctcccttcgc 1200
catgttttac cagtctgtt ttataaccc ttaggttta tcccttaattt tccagcctt 1260
tagtttagt tctgttaacag aacaagttag tctggatga agtctcaaa gtacttcaaa 1320
tggtaattgt ttgttttg taatagctt acaaataaac cttagtttc tatattaaa 1380
aaaaaaaaaa aaaaaaaaaa aaggtacctg ccataataat attctgc 1427

```

(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2639 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vi) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ccctataccctt accctttcccg atttcctttt tttcttttct ttttttatat ggctttttc 60
ttttcttct ttctttttc ttccccttt tatttgacca gtgtaaataa caaacattha 120
ttgggtcacat ttatggtaa aaaaacttcc tacaccagat gcacatgacc cagttttaa 130
atagaacatt ttgaagggtga acacacaccc taacccaggt ttttacccg ctttttaaga 240
tggcaatcc ttcttctccc cccccaccba agacatgtga gcaactgcta atgaaaagca 300
gtaaacagcc gcttaggcta tagcagtcc aactccactc tgaggtgaag attccaatta 360
cattcgagac ttaagtctt tcaattttt cctaacaaaa gttcctgagt ccagtattta 420
caatattaca gcacttagcag atcagtgtct acaactcatc ttttctgct gtatccctt 480
caccagttgg gggagggcct gcacttccat agagtttgc gataatttgt tgaacaattt 540
cttccagttc ctctttctta gctttgaagt cttaatgtc agcatctgg tggcttcca 600
gccattcaat ctctttctt acagttttt ccatggtctc cttatcttca gaggaaagtt 660
tacctccctt gtttcttta tctccaaatct gatttttag agaatagca tagcttcca 720
actcttttctt agtataatcg cgctccttga gcttttgtc ttcctcagca aacttctcag 780
catcattaaac catccttctg atttcttcag gtgcaggcgtt attcgggtca ttggtgattt 840
tgatcttatt tttttccctt gtacccttgt cttagctgt cactcgaaga ataccattca 900
catctatctc aaaggtgact tcaatctgtg ggaccccaac aggagcagga ggaattccag 960
tcagatcaaa tgtaaccaga agatgattt cttttgtcgg ggtctttca ctttcatagal020
ccttgattgt aacagttgg tgattatcag aagctgtaga aaagatctga gacttcttgg1080
taggcaccac tggtttctt ggaatcagg tggcatgac acctcccaaca gtttcaatacl140
aaagtgtaaag gggacataca tcaagcagta ccaggtcacc tggatcttga tcaccaagagal200
gcacaccaggc ctggacagca gcaccatcag ctacagttt atctgggtt atgcacagggl260
atggttccctt gccattgaag aactctttaa ccagttgtc aatcttggg attcggatcg1320
agccaccaac aagaacaatt tcatcaatat cagacttctt ctttccaaacal380
ctttctggac gggcttcata ttagaccggc acagatccat ggctctcaggaa aatcttggg attcggatcg1440
cccgagtcag ggtctcagaa aagtcttctc cttcatagaa ggactcaatt tcaattcttgg1500
tttgcgtcgt agaagacagg gcccgttgg cttttctac ctcgcgcggg agtttctgca1560
cagctctatt gtctttctg acatcttgc cctttctt tttgtacagt ttgtatgaaat1620
tttccatgac acgctggta aagtcttctc caccaggatg agtatctcca ttatggccal680
aaactctgaa gacaccatgg tcaatggta gaagagacac atcgaagggtt ccgcacccca1740
gttcaaacac caggatgttc ttcttccctt cccttcttac caggccataa gcaatagcag1800
tgcctgtagg ctcgttgcgt atccctataa catttaggcc agcaatagt ccagcttctt1860
gggtgtctt gcgttgggca tcattaaaat aggctggta agtaacaact gcatggtaa1920
cttctttcc caaataagcc tcaagcgggtt ctttcatttt agtgagaacc atggcagaaal1980
tttttcagg agcaaattgtc ttgttggc cacccttcaat atcaacttga atgtatggtt2040
agttttctt ttcaaccacc ttgaacggca agaacttgcgt gtcctgtgc acagacgggt2100
attccacgt gggccgcgt agccgcgttgg cgttcaaaagac cgttgcgtcgg ggggtggagg2160
gagctgggt cttggcggca tcgccaatca gacgttcccc tttaggagt aaggcgcacat2220
ggacggcgt gatgcgggtt ccctgtatcgt tggcgatgtt cttccacccggg ccgttcttga2280
cacggccgac gcaggagtagt gtggtccccca ggtcgatgcc gaccaccgtt cccacgttcc2340
cttcttgc ctccttctcg gcccgcgcgg cgctgagcag cagcagcata gggccacca2400
ggagagctt catcttgcca gcaagttggg cagcagcagg cagttccagcc agacggcgt2460
cacaggagc acagcgcata ttccgacttgc caggcggcag gggcccgccc tcacaaggcg2520
cacgaacca ggcgaaggc aggtctagaa atacaggccg cggcgcttcc ctctcacact2580
gcgaaacac cccaaataggt caatctgtct gtgtcttgc ggcggqcatc qacccttaq 2639

(2) INFORMATION ON SEQ ID NO. 114:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 634 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

ctccccgcgcg cgcggttaaa tccccgcacc tgagcatcg 60
ggccatagca ccatgcgtgc ttgtcgccca ggccccctag ccgcggccct cctcctcagc120
ctgtgtgtgt tcgggttcac cctagtctca ggcacaggag cagagaagac tggcggtgtgc180
cccggagctcc aggctgacca gaactgcacg caagagtgcg tctcgacacg cgaatgcgcc240
gacaacctca agtgctgcag cgcgggctgt gccaccccttct gctctctgcc caatgataaq300
gagggttcctt gccccccaggtaa acatccatcattttttccacg tcggccctctg tcgggaccag360
tgcccaaggatgg acaggccatgt tcctggccacg atgaaatgtt gcccgaatgg ctgtggaaag420
gtgtccctgtg tcactcccaa tttctgagct ccagccacca ccaggcttag cagtgaggag480
agaaaatttc tgcctggccc tgcattgtt tccagccac ctgcctccccc cttttcggg540
actctgtattt ccctttggg ctgaccacag cttctccctt tcccaaccaa taaagtaacc600
actttcagca aaaaaaaaaaaaaaaa aaaaaaaaaaca aaaa

```

634

(2) INFORMATION ON SEQ ID NO. 115:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 719 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:
 (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

gtcgactttt tttttttttt tttaacatgg aaaagtattt ttaaaaatcg aataatccct 60
ttcaagtcaa ccagtgtaa cccccgtgtg ctctctgcct gtctgttctt ccccatggga120
gtcacacaaa atgaaaaatct cctagaaga gaagacaag acccgcaaaa gatgtatgcc180
accatctatg agctgaaaga agacaagagc tacaatgtca cctccgtctt gtttaggaaa240
aagaagtgtg actactggat caggactttt gtccaggtt gccagccccgg cgaggtcacg300
ctgggcaaca ttaaagagtta ccctggatta acgagttacc tcgtccgagt ggtgagcacc360
aactacaacc agcatgttat ggtgttcttc aagaaagttt ctcaaaacag ggagtaacttc420
aagatcaccc tctacgggag aaccaggag ctgacttcgg aactaaagga gaacttcatc480
cgcttcctcca aatctctggg cctccctgaa aaccacatcg tcttccctgt ccaatcgac540
cagtgtatcg acggctgagt gcacaggtgc cgccagctgc cgccaccatgc cgaacaccat600
tgagggagct gggagaccc ccccacagtgc ccaccatgc agctgctccc caaggccaccc660
cgctgatgga gccccaccc tctgtctaaa taaacatgtg ccctcaaaaa aaaaaaaaaa 719

```

(2) INFORMATION ON SEQ ID NO. 116:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 494 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

gtcgataacg ccagacgcaa gacgcccggc ctacagcggg agcgtgagga aagccgtgcg 60
ttgcgttcca aggcatctgt gagcccgccg agtatacacc atgagcaaag ctcacccctcc120
cgagttgaaa aaatttatgg acaagaagg atcattgaaa ttaaatggtg gcagacatgt180
ccaaggaaata ttgcggggat ttgatccctt tatgaacctt gtgatagatg aatgtgtgga240
gatggcgaact agtggacaac agaacaatat tggaatggtg gtaatacggag gaaatagtat300
catcatgtta gaaggccttgg aacgagttata aataatggct gttcagcggaa gaaaccatg360
tcctctctcc atagggcctg ttttactatg atgtaaaaat taggtcatgt acatttcat420
attagacttt ttgttaaata aacttttgta atagtcaaaa aaaagtttgg tctcatctac480
cttataatat ctgc                                         494

```

(2) INFORMATION ON SEQ ID NO. 117:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

acggggctga ctacgctcaa agctccattt ttagatcctt tctgtcctcc ttccctggctc 60
ctcccttcctc cccacccttc taataggctc ataagtgggc tcaggcctct ctgcggggct 120
caactctgcgc ttcaccaatgg ctttcattgc caagtccttc tatgacctca gtgccatcag 180
ctctggatggg gagaaggtag atttcaatac gttccggggc agggccgtgc tgattgagaa 240
tgtggcttcg ctctgaggca caaccacccg ggacttcacc cagctcaacg agctcaatg 300
ccgctttccc aggcgcctgg tggtccttgg ctcccttgc aaccaatttg gacatcagga 360
gaactgtcag aatgaggaga tcctgaacag tctcaagtat gtccgtcctg ggggtggata 420
ccagggccacc ttcacccctt tccaaaaatg tgaggatgat gggcagaacg agcatccctgt 480
tttcgcctac ctgaaggaca agctcccccta cccttatgat gaccctattti ccctcatgac 540
cgatccccaa ctcatcattt ggagccctgt gcgcgcctca gatgtggcct ggaactttga 600
gaagttcctc atagggccgg agggagagcc cttccgacgc tacagccgca ccttcccaac 660
catcaacatt gagcctgaca tcaagcgcct ccttaaaggat gccatataaga tgtgaactgc 720
tcaacacaca gatctcctac tccatccagt cctgaggagc cttaggatgc agcatgcctt 780
caggagacac tgctggacct cagcattccc ttgatatcag tcccttgcac tgcagagcct 840
tgcctttccc ctctgcctgt ttccctttcc tctcccaacc ctctgggtgg tgattcaact 900
tgggctccaa gacttggta agctctggc cttcacagaa tgatggcacc ttccctaaacc 960
ctcatgggtg gtgtctgaga ggcgtgaagg gcctggagcc actctgcttag aagagacca 1020
taaaggccag gtgtggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa                                         1065

```

(2) INFORMATION ON SEQ ID NO. 120:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

ggactgcggcgt cgtagtctc cggcgagttg ttgcctggc tggacgtgg tttgtctgct 60
gcccgcgtc ttcgcgtctt cgtttcattt tctgcagcgc gccagcagga tggcccacaal20
gcagatctac tactcgacaa agtacttcga cgaacactac gaggaccggc atgttatgtt180
acccagagaa ctttccaaac aagtacctaa aactcatctg atgtctgaag aggagtggag240
gagactttggt gtccaaacaga gtcttaggctg gtttcattac atgattcatg agccagaacc300
acatattctt ctcttttagac gaccttttcc aaaagatcaa caaaaatgaa gtttatctgg360
ggatcgtcaa atctttttca aatttaatgt atatgtgtat ataaggtgtt attcagtgaa420
tacttggagaa atgtacaaat ctttcatcca tacctgtgca tgagctgtat tttcacagc480
aacagagctc agttaaatgc aactgcaagt aggttactgt aagatgttta agataaaaat540
tcttccagtc agtttttctc ttaagtgcct gtttgagtt actgaaacag ttacttttg600
ttcaataaaag ttgtatgtt gcattaaaaa aaaaaaaaaa aaagtctga 648

```

(2) INFORMATION ON SEQ ID NO. 121:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1842 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

ctgcagccgc tcgagccgct gctctctgga gggggtagag atcaaaggcg gctccttccg 60
 acttctccaa gagggccagg cactggagta cgtgtgtcct tctggcttct acccgtaacc 120
 tgtgcagaca cgtacctgca gatctacggg gtcctggagc accctgaaga ctcagaccca 180
 aaagactgtc aggaaggcag agtgtcagagc aatccactgt ccaagaccac acgacttgcg 240
 gaacggggaa tactggcccc gggtctcccta ctacaatgtg agtgatgaga tctctttcca 300
 ctgctatgac gggtacactc tccggggctc tgccaatcgc acctgccaag tgaatggccg 360
 gtggagtggg cagacagcga tctgtgacaa cggagccggg tactgctcca accccggcat 420
 ccccattggc acaaggaagg tggcagccca gtaccgcctt gaagacagcg tcacctacca 480
 ctgcagccgg gggcttaccc tgcgtggctc ccagcggcga acgtgtcagg aaggtggctc 540
 ttggagccgg acggagccctt cctgccaaga ctcccttcatg tacgacaccc ctcaagaggt 600

ggccgaagct ttccctgtctt ccctgacaga gaccatagaa ggagtgcgtg ctgaggatgg 660
 gacggccca ggggaacaac agaagcggaa gatcgctctg gacccttcag gctccatgaa 720
 catctacctg gtgtcaatgt gtcagacag cattggggcc agcaacttca caggagccaa 780
 aaagtgtcta gtcaacctaa ttgagaaggt ggcaaggat ggtgtgaagc caagatatgg 840
 tctatgtaca tatgccacat accccaaaat ttgggtcaaa gtgtctgaag cagacagcag 900
 taatgcacac tgggtcacga agcagctcaa tgaaatcaat tatgaagacc acaagttgaa 960
 gtcaggact aacaccaaga aggcctcca ggcagtgtac agcatgtga gctggccaga 1020
 tgacgtccctt cctgaaggct ggaaccgcac cggccatgtc atcatctca tgactgatgg 1080
 attgcacaac atgggggggg accaattac tgcattgtat gatgtctatg tggttgggt 1140
 cattggcaag gatgcacaaa accaaggga ggatccggg acttgctata 1200
 cgggccttttgcgtgaaccaag tgaacatcaa tgctttggct tccaagaaag acaatgagca 1260
 acatgtgttc aaagtcaagg atatggaaaa cctggaaatg gtttcttacc aaatgatcga 1320
 tgaaagccag tctctgagtc tctgtggcat ggtttggaa cacaggaagg gtaccgatt 1380
 ccacaagcaa ccatggcagg ccaagatctc agtcattcgc ccttcaaagg gacacgagag 1440
 ctgtatgggg gctgtgtgt ctgagttactt tgcgtgtaca gcagcacatt gtttca 1500
 ggatgacaag gaacactcaa tcaagggtcag cgttaggagg gagaagcggg acctggagat 1560
 agaagtagtc ctatttcacc ccaactacaa cattaatggg aaaaaagaag caggaattcc 1620
 tgaattttat gactatgacg ttgcctgtat caagctcaag aataagctga aatatggcc 1680
 gactatcagg cccatttgct tcccctgcac cgagggaaaca actcgagct tgaggcttcc 1740
 tccaaactacc acttggcagg aacaaaagga agagctgctc cccgcagaag agcaaagaaa 1800
 gctgtgttttgcgttgatggggaa gaaaaaaaaacc gccccgggggg gg 1842

(2) INFORMATION ON SEQ ID NO. 122:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1596 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

- (vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

ggcgggtata aaagccccac ccaggccagc cggctctgct cagcatttg ggacgctctc 60
agctctcgcc gcacggccca gtttccttca aaatgtctac tggcacgaa atcctgtgca 120
agctcagttt ggagggtgtat cactctacac ccccaagtgc atatgggtct gtcaaagcct 180
atactaacat ttgatgtctgg cgggatgcct tgaacatttga aacagccatc aagaccaaag 240
gtgtggatgtat ggtcaccattt gtcaacattt tgaccacccg cagcaatgca cagagacagg 300
atattgcctt cgcctaccat agaaggacca aaaaggaact tgcatacggca ctgaagtctg 360
ccttatctgg ccacctggag acgggtatatt tgggccttta gaagacacat gtcagtatg 420
acgcttctgtat gctaaaagct tccatgaagg ggctggaaac cgacgaggac tctctcattt 480
agatcatctg ctccagaacc aaccaggagc tgcaggaaat taacagatc tacaaggaaa 540

tgtacaaagac tggatctggag aaggacatata tttcggacac atctgggtgac ttccgcaagc 600
tggatgggtgc cctggcaaaag ggttggaaagag cagaggatgg ctctgtcat tattatgttgc 660
tgtatggatcca agatgtctgg gatctctatg acgttggatgtt gaaagaggaaa ggaactgtatg 720
ttcccaatgtt gatcagcattt atgaccggacgg ggagggggccc cacctccaga aagtatatttgc 780
taggtacaaatg agttacatggcc ctttatgtatcat gttggaaagc atcaggaaatg aggtttaaagg 840
agacatgtggaa aatgttttcc tgaaccttggg tcaatgtcattt cagaacaatgc ccctgtatatttgc 900
tgcgtatgttgc ctgtatgtactt ccatggaaagg caagggggacgg cggatataagg tcctgtatgtatg 960
aatcatgttgc tccccggatgtt aagtggacat gttggaaaattt aggttctgtat tcaagagaaaal020
gtacggcaag tccccgtactt attatatccat gcaagacactt aaggggcgactt accagaaaagc1080
gtgtgtgttac ctgtgtgggtt gagatgtactt aagccccgaca cggcctggac gtccagaaaat1140
ggtgcttaccat atgtttccat ctaacatgttcc tggatggaaatccat gcttgcgtat aacagtcccc1200
gtggccatcc ctgtgtgggtt gacgtttagca ttaccccccac ccttcatatgtt gttgcctaag1260
cattgtctgg ctttctgttca tagtctctcc tggatggccaa agaaatgttacat tccatggat1320
gttgaaatgtt aagtgttatgtt tggatggacat tttgtttccat gtgtactgttgc tccatggat1380
atgtatggatgtt tggatggatgtt acgttacttttgc tggccctgttgc tccatggat1440
ttgtttgttgc atggatgttgc tttgggggttgc agtgggtgttgc gctgtccctgttgc tagggaaaal500
gttctggacat tggatgttgc agtggatgttgc cccctatccat gttgtcgatc tttatggat1560
atgtatggatgtt aatggatgttgc aatggatgttgc aaaaaaaa 1596

```

(2) INFORMATION ON SEQ ID NO. 123:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

gtcgcagctg accctcgctc ccggcccccgc ctggagtcgg acgtggaaat tgctggctga 60
ctgggcttgc gagaaacccg cctcgagct gcagccaaag gcaaggaatc actgaagatc 120
ggcgaggggag gacaggggggt tcatcatggg tggcttttc tcaagtatat tttccagttct 180
gtttggact cggaaatga gaattttaaat ttgggatta gatggagcag gaaaaaccac 240
aattttgtac agattacaag tgggagaatg tgtaactact atacctacca ttggatttaa 300
tgttagagacg gtgacgtaca aaaaccttaa attccaagtc tgggatttag gaggacagac 360
aagtatcagg ccatactgga gatgttacta ttcaaaca gatgcagtca tttatgtatg 420
agacagtgtt gaccgagacc gaattggcat ttccaaatca gagttatgtt ccatttttgg 480
ggaagaagag ctgagaaaag ccattttatgt ggtgttgca aataaacagg acatggaaaca 540
ggccatgact tcctcagaga tggcaaattc acttgggtt cctgccttga aggaccgaaa 600
atggcagata ttcaaaacgt cagcaaccaa aggcaccggc cttgatgagg caatggaatg 660
gttagttgaa acattaaaaa gcagacagta attcagttca ttcttctccc ctgaaatgaa 720
gactacatca cctctctccc ttggaaaca gtcaagtta cttcacacta cttagatgtt 780

aaactataatg attattggca tataactgact gactgcaata ttgttagtaa atagggaaaa 840
taatgttttta gttggaggga taatttgatc gaatcacctg aatgttttat gtaatgtaaa 900
atattttttt cttgtttct tttgtttaagg tatataatct attttgtatgg aatttttttatt 960
caaatacagt ttttattaaag agtataactcc tattggatga aaaaaaccta aaaaaaaaaaa 1020
aaaaaaaaaaa aaa 1033

```

(2) INFORMATION ON SEQ ID NO. 124:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ICLLVHFVSR AKTVNLTFSY WWWVITENKDL FSCSLLKSHK NNQIGSCLLS CVSWFLTCVH60
 TPVCL 65

(2) INFORMATION ON SEQ ID NO. 125:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 64 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ISVFRLFKYL THFQTCTMFY KPLDFQQHTI ENTCYSKHNF SVSSIAVV RD NIAISGMLQA60
 FKIA 64

(2) INFORMATION ON SEQ ID NO. 126:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 61 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

KANLLPATPE GTQIWVGPF QLGKRMGKPG DGFHKFSSGL WHSFQEIPLG KGLLANMHFQ60
 T 61

(2) INFORMATION ON SEQ ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

LKNTNEVKAL NWYTLFTPQ QVWKCIFASR PLPRGISWKE CHNPLENLWK PSPGFFIRLP60
 SWKTGPTHIW VPSGVAGRRF AF 82

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

HTWDPPYPLGI SPRTIRPVQCQ PKVAFGMLNF PLSKKVHLPN EVTIRLNPKK SLDFVFYKNS60
 TFPPIKSLVIK ISTLPKCDST AWFLANKNPI 90

(2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

MVADYGCTIL ILGPFTHRNH TKWPDTYFTE QFKYYTLAKS TYSTHPGEgg EKTHTYKTTs60
LDTMCLPTIS SLNNFHQLRC LV 82

(2) INFORMATION ON SEQ ID NO. 130:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 70 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

RNLVTQMKSG IEDPWTWQVN ADYSLAFPLY LCKEGYTELI LFQAYNFKFY HLNSSTFAAE60
EWNQKNVVSW 70

(2) INFORMATION ON SEQ ID NO. 131:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 60 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AIQCEAYFIA TLVDCQGDsa TVLDKLMFPF SLAANRRATy SAGSRARSWG SRGYTSSLII60

(2) INFORMATION ON SEQ ID NO. 132:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 181 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

I PNMAAPLGG MFSGQPPGPP QAPPGLPGQA SLLQAAAGAP RPSSSTLVDE LESSFEACFA 60
 SLVSQDYVNG TDQEEIRTGV DQCIQKFLDI ARQTECFFLQ KRLQLSVQKP EQVIKEDVSE120
 LRNELQRKDA LVQKHLTKLR HWQQVLEDIN VQHKKPADIP QGSLAYLEQA SANIPAPLKP180
 T 181

(2) INFORMATION ON SEQ ID NO. 133:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 423 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

LSEDEIRTLK QKKIDETSEQ EQKHKETNNNS NAQNPSEE EGEGDEDILPL TLEEKENKEY 60
 LKSLEIIL MGKQNIPLDG HEADEIPEGI FTPDNFQALL ECRINSGEV LRKRFTTAV120
 NTLFCSKTQQ RQMLEICESC IREETLREVR DSHFFSIITD DVVDIAGEEH LPVLVRFVDE180
 SHNIREEFIG FLPYEADAEI LAVKFHTMIT EKWGLNMEYC RGQAYIVSSG FSSKMVKVAS240
 RLLEKYPQAI YTLCSSCALN MWLAKSVPVM GVSVALGTIE EVCSFFHRSP QLLLELDNVI300
 AVLQNSKER GKELEICHGS QWTGRHDAFE ILVELLQALV LCDGINSDT NIRWNNYIAG360
 RAFVLCSAVS DFDFIVTIIV LKNVLSFTRA FGKNLQGQTS DVFFAAGSLT AVLHSLNEVS420
 GKY 423

(2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 237 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

VENIEVYHEF WFEETNLAT KLDIQMKLPG KFRRAHQGNL ESQLTSESYY KETLSVPTVE 60
HIIQELKDIF SEOHLKALKC LSLVPSVMGQ LKFNTSEHH ADMYRSIDLBN PDTLSAELHC120
WRIKWKHRGK DIELPSTIYE ALHLPDIKFF PNVYALLKVL CILPVMKVEN ERYENGRKRL180
KAYLRNLTQD QRSSNLALLN INFEDIKHLD LMVDTYIKLY TSKSELPTDN SETVENT 237

(2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

- RIRINGSLCP QTKNNLFHI VELSISGASV GERWYGMGES ILPARGESQG LLCLFYKEI60
LPLFLVNKL GTDVGLEQGL SGGEWSWA 89

(2) INFORMATION ON SEQ ID NO. 136:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

SEERAKREEL ERILEENNRK IAEAQAKLAE EQLRIVEEQR KIHEERMKLE QERQRQQKEE60
82
QKIILGKGKS RPKLSFSLKT QD

(2) INFORMATION ON SEQ ID NO. 137:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

SALKVEYLLS CPVSCRVCSS AAIRASFLFK MICTVSLAIP ASAAQPFIKK QHTRKAELRN60
ADVYGYKKEQK M 71

(2) INFORMATION ON SEQ ID NO. 138:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 67 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

SSAQRKYFNL PVEILVMERC QTVLNGRTSK SEATVPTTRG LLYCSTFSAL YFLAEASPWS60
67
AMYKLGY

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

RAEKVEQYKS PRVVGTVASL LLVLPFKTVW HLSMTRISTG RLKYFLCAE

49

(2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

SCERRGFIMA DDLKRFLYKK LPSVEGLHAI VVSDRDGVPV IKVANDNAPE HALRPGFLST 60
FALATDQGSK LGLSKNKSII CYYNTYQVVQ FNRLPLVVSF IASSSANTGL IVSLEKELAP120

LFEEELRQVVE VS

132

(2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

QMILLFLES P SLLPWSVARA KVDKKPGRKA CSGALSFATL ITGTPSLSDT TMAWSPSTLG 60
 NFLYKNRFRS SAMMNPLLSQ DQSPRLGFLG CLVLSAVTSG TALKTGSSSS HRHMIHDLC120
 APGSTF 126

(2) INFORMATION ON SEQ ID NO. 142:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

SAVKRGWDLN MAAVVAATAL KGRGARNARV LRGILAGATA NKASHNRTRA LQSHSSPEGK 60
 EEPPEPLSPEL EYIPRKRGKN PMKAVGLAWA IGFPCGILLF ILTKREVDKD RVKQMKARQN120
 MRLSNTGEYE SQRFRASSQS APSPDVGSV QT 152

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ECRSAPQVCT PDPTSGDGAL WEEALNLWLS YSPVLDNRMF CRAFICFTRS LSTSRLVRMK 60
 RRIPQGKPMA QASPTAFMGF LPLFLGMYSS SGDRGSGSSL PSGELWLRCRA RVLL 114

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 267 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

EDEVEEEESTA LQKTDKKEIL KKSEKDTNSK VKPKGVWRWT GSRTGRWVY SSNDESEGSG 60
 SEKSSAASEE EEEKESEEEAI LADDDEPCKK CGLPNHPELI LLCDSGDSY HTACLRPPLM120
 IIPDGEGWFCP PCQHKLLCEK LEEQLQDLDV ALKKKERAER RKERLVYVGI SIENIIPPQE180
 PDFSEDQEEK KKDSKKSKAN LLERRSTRTR KCISYRFDEF DEAIDEAIED DIKEADGGV240
 GRGKDISTIT GHRGKDISTI LDEKIIT 267

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 185 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

SSEKSGSCGG MMFSILIPTY TKRSFLRSAR SFFFKATSKS CNCSSNFSQS SLCWQGGQNH 60
 SPSPGMIIIRGG RROAVWYPLS QESHRRRISSG WFGRPHFLHG SSSSARMASS LSFSSSSSEA120
 ADDDFSLPDPS LSSLLEYFHL PRVREPVHRT LPLGFTLEFV SFSDFFKISF LSVFCKAVDS180
 SSTSS 185

(2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 134 amino acids
 (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

KRQPTSAMKD PSRSSTSPSI INEDVIINGH SHEDDNPFAE YMWMENEEEF NRQIEELWE 60
EEFIERCFQE MLEEEEHEW FIPARDLPQT MDQIQDQFND LVISDGSSLE DLVVKSNLNP120
NAKEFVPGVK YGNI 134

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

HSDKRAFTIK SSNTAFTVWK LCYIHQKRAP STQIFPYFTP GTNSFAFGFR LLLTRSSRE 60
EPSLITRSLN WSWIWSIVCG RSAGINHSC SSSSSSISWK QRSINSSSHN SSSICLLNSS120
SFSIHMYSAN GLSSS 135

(2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

LVSGANQCGS CNSKSFLTAKA WYYRVGFRFF RGGLFDFDEF FFYVIFGKTH SELYLVST 58

(2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

FFVLKSLLVG ACYWEQVFVQ KLQSESLCIT ETLFITSLLS LPQKTVGLNK IICILIYLKC60
L 61

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

SACKFLRDLP LLTVDQLMYT CIIKALNKS L WLITAKMGTR HLLCVLVTAV ALRAVRPCLI60

(2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids

(B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

KRDIIILNVFS QRSHKRKKNQ NQINHHEKNE TPHGNTKLWL GSSYYYSSHG GWRRKP 56

(2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

IPVHRLHGRA DPLGWSIVSD LITSGLGAGV LRGLPARRLH SLGRRVLGRP GVWLERLGHG 60
 RRDALGAWSA AQRPRTPGRP ACVCAPRRGP ESPSADPVPP PGRAGDPSPPP DASASGPRGG120
 AATKAGPAHD PGQLRPELRV LPPPPRGDRE 150

(2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

LPVAAGGRQQ DAQLRPELSG VVSRPRLGGG APSRSRGRRRI GWARVSSPAG RRDRVCGGGL60
GASAGRAHAG GAARGAGPLR G 81

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 214 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

PGSQSVTPPM AEPLQPDPGA AEDAAAQAVE TPGWKAPEDA GPQPGSYEIR HYGPAKWVST 60
SVESEDWDSA IQTGFTKLNS YIQGKNEKEM KIKMTAPVTS YVEPGSGPFS ESTITISLYI120
PSEQQFDPPR PLESDFVIED RAEMTVFVRS FDGFSSAQKN QEQLLTASI LREDGKVFD180
KVYYTAGYNS PVKLLNRNNE VWLIQKNEPT KENE 214

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 62 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

PNFYRGFIFN LTMCGGLSCL NLFRAVCSVH QMGRSGMGHL RPFRSGLNRM LEPRLDSDL60
RF 62

(2) INFORMATION ON SEQ ID NO. 159:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 104 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

IHLPKKLISF YLRGEVQFSF GSSESKHLIC WVVWKPFLAF YVLSHNNNSIK QEGKQKTKKK 60
 KGKKKNLHGL VSLTKHVGVAV CLGGAGYRTC QCLGFSINLA RDIK 104

(2) INFORMATION ON SEQ ID NO. 160:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

SLLISRKIKQ NTSPARLTCV YYIYIKQRATP TSQQLGEISA VHAVVCQFGE ITPWKNWKNL60
 LAGKNSFICI KSVLQKNPCG 80

(2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

PSIDLEAEEES QRLLKVVMWF SFKKLLFLES RIYGYNVCSL FVHKIKPFKK LKKKKKRGEK60
KREKGKGKRK RRGEET 75

(2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

KYLTLPYKLL VPFCIPPSIT LTKGIFYCKE YFILYITSHE FLPLVTIQML PSAIIQIAQP60
FYVHNSLL 68

(2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

LFFLFRYHTV PLPPKGRVLI HWMTLCQTQM KLMAIPLVFQ IMFGILNGLY HYAVFEETLE60
KTIHEE 66

(2) INFORMATION ON SEQ ID NO. 166:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 159 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

TRLGDRGGV HFLKALRRGG LRASLLYLL KYRLVFLSSI CVRGMVSSVK SFLVGEQLLS 60
 ISEPRFKMSV CKCSFLSTTS TFVPISSDSK KVSSYFSLCS ESLAEQNLFM MPEVFCSEQK120
 FDPELNDLSF FFTRLFSSLV TLRVSPHAPA SEMQTVLSS 159

(2) INFORMATION ON SEQ ID NO. 167:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 439 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

KSLLFTSSKF PLISFSSPQG LKFRSKSSLA NYLHKNGETS LKPEDFDFTV LSKRGIKSRY 60
 KDCSMAALTS HLQNQSNNSN WNLRTRSKCK KDVFMPPSSS SELQESRGLS NFTSTHLLLK120
 EDEGVDDVNF RKVRKPKGKV TILKGIPIKK TKKGCRKSCS GFVQSDSKRE SVCNKADAES180

EPVAQKSQLD RTVCISDAGA CGETLSVTSE ENSLVKKER SLSSGSNFCS EQKTSGIINK240
 FCSAKOSEHN EKYEDTFLES EEIGTKVEVV ERKEHLHTDI LKRGSEMDNN CSPTRKDFT300
 DTIPRTQIER RKTSLYFSK YNKEALSPPR RKAFFKWTPP RSPFNLVQET LFHDPWKLLI360
 ATIFLNRTSG KMAIPVLWKF LEKYPSEAEGA RTADWRDVSE LLKPLGLYDL RAKTIVKFSD420
 EYLTKQWKYP IELHIGIGAP 439

(2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 90 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

DCGKVQTQMQ FALTNFLGLI SLCKTPVLSF LPQDRVQSFL KHALRCPHLR KCFVDTLKGV60
HKAKKSDQML RASNLYLTTW TWHWQKSLQH 90

(2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 92 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

SDFCQCHVQV VRYKLLALSI WSDFFALWTP LRVSTKQCLR CGHLRACFRK LCTLSCGRKE60
RTGVLHKEIS PRKLVNANCI CVCTLPQSYI VF 92

(2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 91 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ADSHQNYIPW PPACVLLARP WLASLTREKD LQKIRLWDHF VCALGMTFFF TPGKPLGLSE60
91
TLWLANHMVS LKVERLSNPP IPREFQSVDV I

(2) INFORMATION ON SEQ ID NO. 171:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 95 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

NGGLNAHLAS ASEFDHSGVQ LIEREEEICI FYEKINIQEK MKLNGEIEIH LLEEKIQFLK60
95
MKIAEKQRQI CVTQKLLPAK RSLDADLAVL QIQFS

(2) INFORMATION ON SEQ ID NO. 172:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 90 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

KTEFGAQLGR HPGTSWLAVI SGSHKFVFAS QQSSFSGIGS FLPVDFVQFL HLVSSSLGYL60
90
FFHKCIFLL Palsaerhyg QIQRQRQLSGH

(2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 102 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

AVRSRGALSL SVGAACGLVA LWQRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60
 SPFHDIPPIYA DKVRHPCFWT QSLYSDQLVL HMNFIICLST SA 102

(2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 73 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

VKRLLCPKTRM PYLICINWNI MKWRYILSFL IFEEDSVLQG EGRGALLGAE AAHSAGVLPP60
 PLPQSHQPAR GAD 73

(2) INFORMATION ON SEQ ID NO. 175:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 130 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

R.RQRKAEPEGA CALGRVGSEC IPEPGARRTA QAAGLRSVSG AANTKVRELK HFRFLGLIIRS 60
 CRSEMEVDAP GVDGRDGLRE RRGFSEGGRQ NFDVRPQSGA NGLPKHSYWL DLWLFILFDV120
 VVFLFVYFLP 130

(2) INFORMATION ON SEQ ID NO. 176:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 62 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ILKMATNFLN KEDRTLNRRI SHLQGTLPFI LHFVTNLQNS INWVGFHPFL AKFLKLNPLV60
 RV 62

(2) INFORMATION ON SEQ ID NO. 177:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 174 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

AVYCILHQHQK VLRLYKRALR HLESWCVQRD KYRYFACLMR ARFEEHKNEK DMAKATQLLK 60
 EAEEEFWYRQ HPQPYIFPDS PGGTSYERYD CYKVPEWCLD DWHPSEKAMY PDYFAKREQW120
 KKLRRESWER EVKQLQEETP PGGPLTEALP PARKEGDLPP LWYIVTRPR ERPM 174

(2) INFORMATION ON SEQ ID NO. 178:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 131 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

PLVPSFPSAV SSTVLSWQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRCMAV 60
 DADGTRILP R PPSAAGWPSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVAPAYKAA120
 TPFADVVCNI R 131

(2) INFORMATION ON SEQ ID NO. 179:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SSWSGVIPFF FSCSCLPFLY60
 PPKWRQIHDL KDTQYLLNSS 80

(2) INFORMATION ON SEQ ID NO. 180:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

KVIRKLKGPE EASGQMGAG PTMLLREENG CCSRRQQSSS AGDSDGERED SAAERARQQL 60
 EADLNKTMRI RMTDGRTLVG CFLCTDRDCN VILGSAQEFL KPSDSFSAGE PRVLGLAMVP120
 GHHIVSIEVQ RESETGPPYL 140

(2) INFORMATION ON SEQ ID NO. 181:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 114 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SLKGKRHRGQ RYGGPVRLSL CTSMETMWCP GTMARPSTRG SPAEKESDGL RNCAEPRMT 60
 LQSRSVQRKQ PTSVRPSVMR MRIVLLSSAS SCCRARSAAE SSRSPSESPA LELL 114

(2) INFORMATION ON SEQ ID NO. 182:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 95 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

RLSRLTEPK EPMAGISTAE HHLDPTAALP TQLSRSRHSP QVISTDGGET RGCGRQERKA60
 ERRVCKNAKV TFPPIVGKQG RHWFCCHRQS EHLEL 95

(2) INFORMATION ON SEQ ID NO. 183:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

RRVQHPPFFS QLIRDAAKRT FRITRLQAFS KYLVVYVYLN GSMLPVPSPC PLCQPPVALV 60
 LVSFPSSAKR PWNLNGGCFA LGGSCWWDQS FDKPPAPWWH LSWKDVTTPG AQTACGSRTS120
 AFGIFLPQWG R 131

(2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TAPCCRCPAP VPSVNPLSLW CWFRSRLQQN DLGTSMGAAL LWEVLVGGR ALTNLLLLGG 60
 TSPGRTSQLQ VLRLPVAAEP VPLAFSSHNG EGDFGILTNS SLGLSLLPST ASRFSSICAY120
 YLRTVSAP 128

(2) INFORMATION ON SEQ ID NO. 185:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

DSRVYCFSGN YRKLVLPRT GAIRNGSNIS KLRKQDVLSF AHLGFLLFPF SLFSLRSLFQ60
 FPSDLPLVPL ESQRL 75

(2) INFORMATION ON SEQ ID NO. 186:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 62 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

LGDSESMPLL ALKCPVRLLG TLEPSEILII LGSSPYFQMF SAQHWVLSST TENPEEKGR60
 FP 62

(2) INFORMATION ON SEQ ID NO. 187:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 89 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

PHPSRRLTQG RWVRKSRVAM EKIPVSAFLR LVALSYNLAR DSTVKPGAKK DRKESRAKLR60
 QTLSRSWGEQ LIWTQTYEEA LYKSRLATN 89

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 72 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GNPELPWRKF QCQHSCALWR SPTIWPGLAQ SNLEPKRTGR SLEPNCARPS PEVGVNNSSG60
 LRRMKKLYIN RD 72

(2) INFORMATION ON SEQ ID NO. 189:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 125 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

SLGHRPRNNGG HSRGCDLGGL HAHSPDPRLQ GAGLQQAKNA AYSVSLPPGC VGHLWPHLRL 60
 HHRTGREHRA HTLLPLWDPL FHLLLPGS CCQSDQARPG EEAPFPVGDS GSGRGLQPSP120
 GCYRY 125

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 200 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

RGRDSCP RSP PALRSSPAAL LRAGSSTKFT ANALALGSRM ATTVPDGCRN GLKSKYYRLC 60
 DKAEGAWGIVL ETVATAGVVT SVAFMLTLPI LVCKVQDSNR RKMLPTQFLF LLGVLGIFGL120
 TFAFIIGLDG STGPTRFFLF GILFSICFSC LLAHAVSLTK LVRGRKPLSR LVLGLAVGF180
 SLVQDVIAIE YIVLTMNRTK 200

(2) INFORMATION ON SEQ ID NO. 191:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 111 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

AEAHGQTQNH QPGKGLPPP D ELGQTDSMSQ QAGEADGKED PKEEEACGPC APVQSDDEGE 60
 GEAKDAQHTQ EEEKLSRQHF SPVGVLHLAD EDRESEHEGH RGHNPGCGHR F 111

(2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 92 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

EIYWETDYNH SGTIDAHEMR TALRKAGFTL NSQVQQTIAL RYACSKLGIN FDSFVACMIR60
 LETLFKLFS LDEDKDGMVQ LSLAEWLCCV LV 92

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ESLIAFLFLH DQCAQDSIVL TMIKDVVRIO WTRNECKGGL EQRRGCPEGK ESYQILLNLQ60
PERLEFHRRPQ SAPFHCSRHI K

81

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

KTTIHGPCQN HLPPPHCFLK RPGTLSKGDP IDSSQEGFRA SIRAWPVLA^P LLSEQQGFQG60
SGWHESLSLP SCSFMTNVPR TQ

82

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

RPPPSSRSSL AGQTNTQHSH SARES

25

(2) INFORMATION ON SEQ ID NO. 196:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TMPSSLSSRR LNSLKRVSRR IIQATKLSKL MPSLLHAYRR AMVCCTWLLR VKPAFLRAVL60
ISWASMVPEW L

71

(2) INFORMATION ON SEQ ID NO. 197:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 86 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

IRRNTSRISW HTWRRTPPYD SPACFSCSIV SLEGSGFFSC VSVFFSFDSL NFSISAISGL60
SDMVAAEKQS EAHEYERQFL ASRRSG

86

(2) INFORMATION ON SEQ ID NO. 198:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

HPFSTFPPTLP PQAGKFDATL LASQCILGGA RLLTIRLLAS PVQSFWKAV DFSLASLSSS 60
VSTYRISRSQ PYRVCQTWLR RKSARRTST SDSSSRRAAV A 101

(2) INFORMATION ON SEQ ID NO. 199:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TPFPPSQLYP LKQVNSTQHF SHLSAYLAHH ASLRFACLLL LFNRFFGRQW IFLLRLCLLQ 60
FPLIEFLDLS HIGFVRHGCG GAKRGARVR ATVPRVSPQW 100

(2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GLTDOYLELN ALQEELGPFG LVLGFPSNQ FGKQEPPGENS EILPSLKYVR PGGGFVPNFQ 60
 LFEKGDVNGE KEQKFYTFLK NSCPPTAELL GSPGRLFWEP MKIHDIRWNF EKFLVGPDI120
 PVMRWYHRTT VSNVKMDILS YMRRQAALSA RGK 153

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 249 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

LMPPPYPYPL PIMQGPRRGS SGRKPHSQSF YPHPRFSFLL HKRQAWHNCV SEPLWTRDNC 60
 PSVCMATQPR ICLLETQGWS ICVYGLAQHP HIFFSFLFQM SPKETQVLGP MVLLKPEHHS120
 WGQHLPHAH T HHQPPSSFL KDPPEPPSPS HSAPETSQDN CERDGRVPQV RGGVSMKEGP180
 EALVGGPPLS PSVVPALSAF RLRLPGRDTT PAPLEDMLSS HSVHWYLNTP ICPVKVFLQQ240
 KKKRKKKKK 249

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 156 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGLSAPPPAP LLCRAQAPLA LGPNFSYRHG VRPGSSPGAH LPEARCGGGP RGRSQAQSPQ 60
 SSGPVGGRGR SGSKARTPQL FRLQQQLQRF GHGCEVPRCW LQAAREHPGQ GQEAQSEEEG120
 EGQESEGQEE GGSPLKGPGQ GSLNLPLCLR VPTTWS 156

(2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:**
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

DPTSLTAMEF DLGAALEPTS QKPGVGAGHG GDPKLSPHKV QGRSEAGAGP GPKQGHHSSS 60
 DSSSSSSDSD TDVKSHAAGS KQHESIPGKA KKPKVKKKEK GKKEKGKKKE APH 113

(2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:**
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

GGPPPPKHLS SRWLVLVGRE EGLMSPVQGP SVGSLLLAL LLLALLLH FGLLGLarda 60
 LVLLGASSVG LHIRVRIAGA AAGVGRAVVS LLWTRTCPCL RPALNFVGTE LGISPVARPH120
 TGLLGGGLQG CSQVELHGGK RSWVLRPRAP GPCRGAEQGE ER 162

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:**
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

VEPWTTCAA GAVMADYWKS QPKKFCDYCK CWIADNRPSV EFHERGKNHK ENVAKRSEI 60
 KQKSLDKAKE EEKASKEFAA MEEAALKAYQ EDLKRLGLES EILEPSITPV TSTIPPTSTS120
 NQQKEKKEKK KKRSPFKGQMG RRHNL 145

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

PALSHLPRHQ INRKKRKRRR KKDP SKGRWV EGITSEGYHY YYDLISGASQ WEKPEGFQGD 60
 LKKTAVKTVW VEGLSEDGFT YYNTETGES RWEKPDDFIP HTSDL PSSKV NENSLGTLD E120
 SKSSDSHS DS DGEQEAE EGG VSTETEKP KI KFKEKNNSD GGSDP ETQKE KSIQKQNSLG180
 SNEEKSKTLK KSNPYGEWQE IKQEVE SHEE VDLELPSTEN EYVSTSEADG GGEPKVV FKE240

KTVTSLGVMA DGVA PVFKKR RT

262

(2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GKGRRKGIGK VCCNGGSCPE SIPRGFEKTW LRVRNFGAKH NTSNQHYPTY LDIKSTERKE60
REEEKKILQR ADG 73

(2) INFORMATION ON SEQ ID NO. 208:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 68 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

IWNFQALKMS MYQLQKLMVA ENPKWYLKKK QSLLLELWQM EWPQSSKREE LENGKILGKF60
KGNEVMIQ 68

(2) INFORMATION ON SEQ ID NO. 210:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 194 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

SVHCFREDKM KFTIVFAGLL GVFLAPALAN YNINVNDNN NAGSGQQSVS VNNEHNVANV 60
DNNNGWDSWN SIWDYGNNGFA ATRLFQKKTC IVHKMNKEVM PSIQS DALV KEKKLQGKGP120
GGPPPKGLMY SVNPNKVDDL SKFGKNIANM CRGIPTYMAE EMQEASLFFY SGTCYTTSVL180
WIVDISFCGD TVEN 194

(2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 82 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

VHQALGRWSS WSLTLKLLFL DQCIKGLNGG HDFLVHFVHN ACLLLKESGC SKAISIIPDG60
IPGVPSVVIV NIGHIVFIVD TH 82

(2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 119 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ELGLNHLWLR VWLEPTAQVP DVLFPEFMER EEKAVSLLLW FNVKEPQLPP LPGREAFGFL 60
LLLLLALVAGE VLQDHRLALQ LVLAGLRAHA GRLRFRKALT KASARCAPEG WTSESFASF 119

(2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 136 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

IICGCVSGLS PLHRSRSLMYCF QSSWRGRKRL YLCCSGLMSK SRSSLCLAE KPLAFFFFSL 60
RLWRVKYSRT TALRCSWSSR ACGLMRGVCA SGRPSRRPRP AVLLKAGHRS HSPLSETMHG120
RSHSSFSDRF RRSLMT 136

(2) INFORMATION ON SEQ ID NO. 214:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TLETVHQGPV QWAQARHAAT DDSGQALKGR SSRGYYFSDK IQMPLLCGYY RNPSTGNKAH 60
FQNYHQRRPP ESYPQAKLRV HCGNRWLYFL HLREQIPASV K 101

(2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LRCPAFRSTA GRGLREGLPE AQTPRMSPQA REDQLQRKAV VLEYFTRHKR KEKKKKAKGF 60
 SARQRRELRL FDIKPSEQRY SLFLPLHELW KQYIRDLCSG LKPDTQPQMI QAKLLKADLH120
 GAIISVTKSK CPSYVGITGI LLQETKHIFK IITKEDRLKV IPKLNCFVFTV ETDGFISYIY180
 GSKFQLRSSE RSAKKFKAKG TIDL 204

(2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 645 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

PTRPVAAGSE QQQQSAFIQE RQPVALMRLL SFNVPHIKNS TGEPIWKVLI YDRFGQDIIS 60
 PLLSVKELRD MGITLHLLLH SDRDPIPDPV AVYFVMPTEE NIDRMQCDLR NQLYESYYLN120
 FISAISRSKL EDIANAALAA SAVTQVAKVF DQYLNFITLE DDMFVLNCQN KELVSYRAIN180
 RPDIRTEME TVMDTIVDSL FCFFVTLGAV PIIRC SRGTA AEMVAVKLDK KLENLRDAR240
 NSLFTGDTLG AGQFSFQRPL LVLVDRNIDL ATPLHTWTY QALVHDVLDL HLNRVNLEES300
 SGVENSPAGA RPKRKNNKKS YDLTPVDKFQ KHKGSPFPEV AESVQQELES YRAQEDEVKR360
 LKSIMGLEGE DEGAISMLSD NTAKLTSAVS SLP ELLEKKR LIDLHTNVAT AVLEHIKARK420
 LDVYFYEERK IMSKTTLDKS LLDIISDPDA GTPEDKMR LF LIYYISTQQA PSEADLEQYK480
 KALTDA GCNL NPLQYIKQWK AFTKMASAPA SYGSTT KPM GLLSRVMNTG SQFVMEGVKN540
 LVLKQQNLPV TRILDNLMEM KSNPETDDYR YFPDKMLRGN DSSVPRNKNP FQEAIVFVVG600
 GGNYIEYQNL VDYIKGKQGK HILYGCSELF NATQFIKQLS QLGQK 645

(2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

GAGPSQLRH YPRISMAVRQ WVIALALAAL LVVDREV PVA AGKLPFSRMP ICEHMVESPT 60
 CSQMSNLVCG TDGLTYTNEC QLCLARIKTK QDIOQIMKDGG C 101

(2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

QLGWIFYFMS YPLHAHHCSP ADTSWLEVLL WDQHLPDFMI WMSCLVFIRA KQSWHSFVYV 60
SPSVPQTRLD IWEQVGDSTM CSQMIGILEKG SFPAATGTSL STTRRAAKAR AITHWRTAML120
ILG 123

(2) INFORMATION ON SEQ ID NO. 219:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

IKAKFNLNAF FFFFLLRSEI GTVILSTERQ TIKWAMKGGG KVLSIVRGIQ PEIKPIYKHV60
CSSK 64

(2) INFORMATION ON SEQ ID NO. 220:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

SFAIPFPWHC TISPIIGQSL GFLGFTMVAT TIRLIDGSNL KKKVMVMDKI SRSREVCYHK60
ITVASTS 67

(2) INFORMATION ON SEQ ID NO. 221:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 117 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

TIISSITDSQ LQEVAEQLLEI FAALHEVLHI INDRKNLKGG LQEVAEQLEL ERIGPQHQAG 60
SDSLLTGMAF FKMREMFFED HIDDAKYCGH LYGLGSGSSY VQNGTGNAYE EEANKQS 117

(2) INFORMATION ON SEQ ID NO. 222:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 196 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

PTCPIQHFIM MKLWVPSRSL PNSPNHYRSF LSHTLHIRYN NSLFISNTHL SRRKLRVTNP 60
IYTRKRSLNI FYLLIPSCRT RLILWIIYIY RNLKHWSSTST VRSHSHSIYR LRPSMRTNII120
LRCHSYKKPP ISHPIYWNNP SRMNLRGLLS RQSHLDPLR FPLHLTIYYR GPSNRSPPLP180
PRNRIKQPNR IKLRCR 196

(2) INFORMATION ON SEQ ID NO. 223:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 174 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

LPSAIEGPTP VSALLHSSTI VVAGIFLLVR FHPLTTNNNF ILTTLCLGA LTTLFTAICA 60
LTQNDIKKII AFSTSSQLGL IIVTLGINQP HLAFLHICHT AFFKAILFIC SGSIIHSLAD120
EQDIRKIGNI TKIIPFTSSC LVIIGSLALTG IPFLTGFYSK DLIEAINTC NTNA 174

(2) INFORMATION ON SEQ ID NO. 224:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 123 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

FLKTTALIIS VLGFIAALEL NNLTIKLSIN KANPYSSFST LLGFFPSIIH RITPIKSLNL 60
SLKTSLTLLD LIWLEKTIPK STSTLHTNIT TLTTNQKGLI KLYFISFLIN IILIIILYSI120
NLE 123

(2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 129 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

NMLLAEVRI S M VIRNSVRYL MNRLMFGSEC IYHEENCIID HVTKRATDVN RIEKKSVLKL 60
ILSSIEFMVT QCQVVIISI LLWKNINRGK RLIMKENLID VVVYSGKLMC LIRFDIEIRI 120
GDSRRMKIK 129

(2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

FFFFFFFAIQ MNVYFLNPHR VRAELRDAWH SISHPGSLPR SFFFAGSILD LYHFLQRQYP 60
EWQSQVYFKV GVFGSRGDW IPS 83

(2) INFORMATION ON SEQ ID NO. 227:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

SMMLFKVLVI TVFCGLTVAF PLSELVSINK ELQNSIIDLL NSVFDQLGSY RGTKAPLEDY 60
 TDDDLSTDSE QIMDFTPAAN KQNSEFSTDV ETVSSGFLEE FTENTDITVK IPLAGNPVSP120
 TS 122

(2) INFORMATION ON SEQ ID NO. 228:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

TSTTVFFFFP HLSLPVGCTV CSHALCINIL EIYRSVLYFL YCWILIITF TRVLNKSSLT60
 RK 62

(2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ARPCMNSTKA LPHGREHTRL KMLSYLKNKM CKSSGWHKTK VNASWGTFLR GLAECSVNIID60
 FCLCYMTSVT SLKICTIQFQ LWITSVDLCE GFYLCRMGV 99

(2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

GELQKSSHYH PPELFEMIFF VHFGCSIGGR IYYNMDHLYF CIYLFITRPQ PQSSFSPSTS60
 63
 LCL

(2) INFORMATION ON SEQ ID NO. 231:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

INKYRSRDDP YYISIFYHQYC SQNVQKKSFQ ITQEDDNGWT FVIHLKDCGR ANSTHCIVCA60
 64
 YGGL

(2) INFORMATION ON SEQ ID NO. 232:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

PLFCAILKTC TFYFSDSLTF LIECVLYHAV MLWYYSYRVL PILKTCHFPK RSFDLAEVL60
 88
 HKLKSLSNIN MKGGTGCNIY SQVTSLYI

(2) INFORMATION ON SEQ ID NO. 233:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 161 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

ASTIMDLLFG RRKTPEELLR QNQRALNRAM RELDREHQKL ETQEKKIIAD IKKMAKQGQM 60
DAVRIMAKDL VRTRRYVRKF VLMRANIQAV SLKIQTLKSN NSMAQAMKGV TKAMGTMNRQ120
LKLPQIQKIM MEFERQAEIM DMKEERIELL HLMIPWVLGK F 161

(2) INFORMATION ON SEQ ID NO. 234:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 120 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

RRVRTKSFAM MRTASIWPCL AIFLMSAMIF FSWVSSFCRS RSSSRMARFR ALWFCRSSSS 60
GVFRRPNNRS MMVEAHWQAG AGTDTRFRFR VTLLFLGSPT CPPTKAPRSC RRRRRFRGRV120

(2) INFORMATION ON SEQ ID NO. 235:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 121 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

KLPQNPRDHQ MQQFNPLLH IHDLCLPLKL HDLDDLGQL QLSVHGAHGL GDTLHGLCHR 60
 VVGLECLDLE GHSLDVGPHQ YKLAHIAPGA HQVFCHDANS IHLALLGHLL NVCNDFLLLG120
 L 121

(2) INFORMATION ON SEQ ID NO. 236:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

KTKRSVKDAA KKGQKDVCIV LAKEMIRSRK AVSKLYASKA HMNSVLMGMK NQLAVLRVAG 60
 SLQKSTEVMK AMQSLVKIPE IQATMRELSK EMMKAGIIEE MLEDTFESMD DQEEMEEEAE120
 MEIDRILFEI TAGALGKAPS KVTDALPEPE PPGAMAASED EGEEEEALEA MQSRLATLRS180

(2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

LMPFQSQNLO ERWLPQRMRG RRKRLWRPCS PGWPHSAARG CLPRWVCTHS SQELPFYVSL 60
 ALHLCEDYH FGEGSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRKKKKK K 111

(2) INFORMATION ON SEQ ID NO. 238:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 103 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

KICERCCQEG PEGCLHSSGQ GDDQVKEGCE QAVCIQSTHE LSAHGDEEPA RGLASGWFP 60
 EEHRSDEGHA KSCEDSRDSDG HHEGVVQRND EGWDHRGDVR GHF 103

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 351 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

TWCCTTMLAA RLVCLRTLPS RVFHPAFTKA SPVVKNSITK NQWLLTPSRE YATKTRIGIR 60
 RGRTGQELKE AALEPSMEKI FKIDQMGRWF VAGGAAVGLG ALCYYGLGLS NEIGAIKEAV120
 IWPQYVKDRI HSTYMYLAGS IGLTALSAIA ISRTPVLMNF MMRGWSVTIG VTFAAMVGAG180
 MLVRSIPYDQ SPGPKHAWL LHSGVMGAVV APLTILGGPL LIRAAWYTAG IVGGLSTVAM240
 CAPSEKFLNM GAPLGVLGL VFVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFSMFLLYD300
 TQKVIKRAEV SPMYGVQKYD PINSMLSIYM DTLNIFMRVA TMLATGGNRK K 351

(2) INFORMATION ON SEQ ID NO. 240:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 147 amino acids
 (B) TYPE: Protein

(C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

RVAPATVVGG RNIDPNEDTK TRPRPTPRGA PMFRNFSLGA HMATVERPPT MPAVYHAALM 60
 RRGPPNIVRG ATTAPITPEC SNQARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120
 MKFMRTGVLL IAMADKAVKP ILPAKYI 147

(2) INFORMATION ON SEQ ID NO. 241:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 196 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

KARRRGTMMAA AADERSPEDG EDEEEEEQLV LVELSGIIDS DFLSKCENKC KVLGIDTERP 60
 ILOVDSCVFA GEYEDTLGTC VIFEEENVEHA DTEGNNKTVL KYKCHTMKKL SMTRTLLTEK120
 KEGEENIGGV EWLQIKDNDF SYRPNMICNF LHENEDEEVV ASAPDKSSEL EEEEIQMNHR180
 FKPGFVEPGE PIAPWE 196

(2) INFORMATION ON SEQ ID NO. 242:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

PPAPALRHRE TRRPVASLHV GTGALGARSH PPAGSRHLEF WQKQFARRGA DGQEPMKLLR 60
 LGAEARTQDG GSGRAWPVTR RRGAAGPWRR RRTSGVQRT KTRKRSSWF WWNYQELLIQ120
 TSSQNVKINA RFWALTLRGP FCKWTAVSLL GSMKTL 156

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 132 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

RRLEVSYRQH HFRVSLAPWS KMADEATRRV VSEIPVLKTN AGPRDRELWV QRLKEEYQSL 60
 IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLLKYE FDIEFDIPIT YPTTAPEIAV120
 PELDGKTAKM YR 132

(2) INFORMATION ON SEQ ID NO. 244:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 159 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

LFAISYSVLP VHLCCLSIQL RNCNFWGSSR ICDRNVKLDV KLIFQEVMDI PAFSKPPSSF 60
 LVGLQSEPIV VSILVVHLIP DKGLIFLLQS LHPQLTISGS GVSLQHRDLR HNTSRGFIRH120
 LGPGRKRNAE VVLPVAYLKA PSSLLWEDET LGCKTSFE 159

(2) INFORMATION ON SEQ ID NO. 245:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 103 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATLPDALPPA TKFLKAFFD SLPSPIQSYL YIFAVFPSSS GTAISGAVVG YVIGMSNSMS 60
 NSYFRRSWIY QHFPNHRVPS LLDSSRNQSL SAFLLFSTYR IRD 103

(2) INFORMATION ON SEQ ID NO. 246:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 285 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

AVRRRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60
 SPFHDIPPIYA DKDVFHMVVE VPRWSNAKME IATKDPLNPI KQDVKKKGKLR YVANLFPYKG120
 YIWNYGAIPQ TWEDPGHNDK HTGCCGDNDP IDVCEIGSKV CARGEIIGVK VLGILAMIDE180
 GETDWKVIAI NVDDPDAAANY NDINDVKRLK PGYLEATVDW FRRYKVPDGK PENEFAFNAE240
 FKDKDFAIDI IKSTHDHWKA LVTKKTNGKR IMLIVQLFVG PLKVC 285

(2) INFORMATION ON SEQ ID NO. 247:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 94 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

TKGLRIAQAO LCPGSPRCS QSISRRACAL CLRSTQPNT TYLRKPGGRK RAVGHKSPA 60
TRVPASVQRS QPPRAHRKSC LASLGLCKNN KCLS 94

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 113 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

DPRPSRIQHI SGNPAGASER LAIRQLKRE YLLQYNDPNR RGLIENPALL RWAYARTINV 60
YPNFRPTPKN SLMGALCGFG PLIFIYYIIK TERDRKEKLI QEGKLDRTFH LSY 113

(2) INFORMATION ON SEQ ID NO. 249:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 98 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

VFRSGSEIRI DIYCSCIGPT KQGRIFDEPS AVGIVVLKQV LSFQLGSYQO PLACARRVSG 60
DMLYSAGSRV SGRVRRLDGL YFGNDILANQ GTIAPARF 98

(2) INFORMATION ON SEQ ID NO. 250:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

TQVMVQSMFA PTDTSDMEAV WKEAKPEDLM DSKLRCVFEL PAENDKPHDV EINKIISTTA 60
SKTETPIVSK SLSSSLDDTE VKKVMEECKR LQGEVQRRLRE ENKQFKEEDG LRMRKTVQSN120
SPISALAPTG KEEGLSTRLL ALVVLFFIVG VIIGKIAL 158

(2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

VNKALPFISK ALGQSVNTRL SLMTSTSAA TVQFLWASDS VHQSQGADGL DRTEDTESSL 60
GREWATWGLL CGADRTPQHA GLQLPKGQHQ QARKGVILRE VIQHHVPRPT NV 112

(2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

SKGCSITETV TVDPGSIIPL LGLTQYRRGA VVFTLKHFL SDGFRNLRFV VTTSVKGPLN 60
 LRSVGGSRTR ICSSSPWPLR RTPSERQRRA GGGLLAGGGG RWREGRGSEF ASLLFLVRLC120
 STTFLCWQIC FQIDF 135

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 189 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

SMQSAVSFFF FSLDQKKICL PTISLWWPT VTIFLCVQRH IGFAFNDLLR LENTIKTNCS 60
 ATGQVVYYQI ITSRCQLHIE SFMKFINKEF FFLCGFNKSS RIVQSLVNVI LIIPLNFICC120
 CYLLKYDLFR LLIPLIQEMP RGIPWGNGAS YSVNFSSFTF ANIMAEFFLS LVRQLLTEFF180
 ILTILSHGI 189

(2) INFORMATION ON SEQ ID NO. 254:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 300 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

KSIWKQICQH KNVVEQSLTR KRRDANSPLP PSRHRPPPA SKPPPALARCL SDGVRLRGHG 60
 EDEQILVLDP PTDLKFKGPF TDVVTTNLKL RNPSDRKVCF KVKTAPRRY CVRPNSGIID120
 PGSTVTVSVM LQPFDYDPNE KSKHKFMVQT IFAPPNTSDM EAVWKEAKPD ELMDSKLRCV180
 FEMPNENDKL NDMEPSKAVP LNASKQDGPM PKPHSVSLND TETRKLMEEC KRLQGEMMKL240
 SEENRHLRDE GLRLRKVAHS DKPGSTSTAS FRDNVTSPLP SLLVVIAIF IGFFLGKFIL300

(2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 247 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSGLK HEDKRGGSGS 60
 HNWGTVKDEL TESPKYIQQKQ ISYNYSLDQ SNVTEETPEG EEEHPVADTE NKENEVEEVK120
 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSKE EAHAEDSVMD180
 HHFRKPANDI TSQLEINFGD LGRPGRRGGR GRGGRGRGGR PNRGSRTDKS SASAPDVDDP240
 EAFFPALA 247

(2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 69 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

FVFDSSPVVR SATSTFVLVL QARSITSTMP IKFTFATRIK SISSAHSTST APSTLFQDH60
 69
 DLESRAARA

(2) INFORMATION ON SEQ ID NO. 257:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 220 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

PGRGSMYDRM RRGGDGYDGG YGGFDDYGGY NNYGYGNDGF DDRMRDGRGM GGHGYGGAGD 60
 ASSGFHGHHF VHMRLGLPFRA TENDIANFFS PLNPIRVHID IGADGRATGE ADVEFVTHED120
 AVAAMSKDKN NMQHRYIELF LNSTPGGGSG MGGSGMGGYR RDGMDNQGGY GSVGRMGMGN180
 NYSGGYGTPD GLGGYGRGGG GSGGGYQQGG MSGGGWRGMY 220

(2) INFORMATION ON SEQ ID NO. 258:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AATGAGCTG GTGTTAGATG AGTTTACAG CTCACTCAGG GTGGTGGGTG TCTCTGCTGT 60
 TCTGGGTACT GGATTAGATG AACTTTGTG GCAAGTTACC AGTGCTGCCG AAGAATATGA 120
 AAGGGAGTAT CGTCCTGAAT ATGAACGCT GAAAAAAATCA CTGGCCAACG CAGAGAGCCA 180
 ACAGCAGAGA GAACAACCTGG AACGCCTTCG AAAAGATATG GGTTCTGTAG CCTTGGATGC 240
 AGGGACTCCC AAAGACAGCT TATCTCCTGT GCTGCACCCCT TCTGATTTGA TCCTGACTCG 300
 ACCAACATTG GAAGCAGACA GCGATACTGA TGACATTGAC CACAGAGTTA CAGAGGAAAG 360
 CCATGAAGAG CCAGCATTCC AGAATTTTAT GCAAGAAATCG ATGGCACAAT ACTGGAAGAG 420
 AAACAATAAA TAGGAGACTT TAGCACACTT CACTTGTTC TAGAAGTCCA GAATTTGGA 480
 CCTCCACGTG AAAGAACTGT TCTTACCTCT GAACCTGGGG CTCCCATAAG GGATAATTT 540
 CCTCAGAGTA GCAAAGTTTC TCTTATTAGA GAAATCTTGT GACTCAGATG AAGTCAGGGA 600
 TAGAAGACCC TTGGACCTGG CAGGTAAATG CTGATTATTTC CTTGGCCTTT CCCTTGTATT 660
 TATGCAAGGA AGGATATACT GAGCTGATAC TCTTCCAAGC CTACAACCTC AAGTTTTATC 720
 ATTTGAACTC AAGTACTTTT GCTGCTGAGG AATGGAATCA AAAGAACGTA GTCTCCTGGT 780
 AACCAACCTCA GATCTCTATT ATTAGGCTAG ATGTATAGCC TCTACTCCCC CAGCTTCTTG 840
 CTCTTGACCC TGCACTGTAA GTTGGCCCTTC TATTAGCAGC CAAGGAAAAG GGAAACATGA 900
 GCTTATCCAG AACGGTGGCA GAGTCTCCTT GGCAATCAAC CAACGTTGCT ATGAAATATG 960
 CCTCACACTG TATAGCTCAT TATAGGACGT CAGGTTGTT GAAAAAAAGTG GGCAAGACAT1020
 GATTAATGAA TCAGAATCCT GTTTCATTGG TGACTTGGAT AAAGACTTT TAATTTAAA1080
 AAAAAAAAAA AAAAAAAAAA AAAAAA 1105

(2) INFORMATION ON SEQ ID NO. 259:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1088 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

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ATTCCAAACA TGGCGGCTCC ACTAGGGGGT ATGTTTCTG GGCAGCCACC CGGTCCCCCT 60
CAGGCCCGC CGGCCCTTC GGGCCAAGCT TCGCTTCTTC AGGCAGCTCC AGGCAGCTCCT 120
AGACCTTCCA GCAGTACTTT GGTGGACGAG TTGGAGTCAT CTTTCGAGGC TTGCTTGCA 180
TCTCTGGTGA GTCAGGACTA TGTCAATGGC ACCGATCAGG AAGAAATTCG AACCGGTGTT 240
GATCAGTGT A TCCAGAACATT TCTGGATATT GCAAGACAGA CAGAATGTTT TTTCTTACAA 300
AAAAGATTC AGTTATCTGT CCAGAAACCA GAGCAAGTTA TCAAAGAGGA TGTGTCAGAA 360
CTAAGGAATG AATTACAGCG GAAAGATGCA CTAGTCCAGA AGCACTTGAC AAAGCTGAGG 420
CATGGCAGC AGGTGCTGGA GGACATCAAC GTGCAGCACA AAAAGCCCGC CGACATCCCT 480
CAGGGCTCCT TGGCCTACCT GGAGCAGGCA TCTGCCAAC TCCCTGCACC TCTGAAGCCA 540
ACGTGAGCAA AGGGCAGAGG CAGTTGGCCT ATGAGTGGGC TGATGCGTGA GGTTGGCCAC 600
ACATTCTTC CTGTGGACTT GACATTTGG AAGAACTCTT TGCCAGATAA TGAGTTCAATT 660
TTAGTTTAT GCTCCATTG AAAAATTTC CACTATTTT ATAAGCTGTT AATTCTTGAA 720
GTACTTTATA ACATGTCTGT AGCTTGGATA AACCAAGTAA GTATTTTTT TTGCTTTA 780
GCGAAGTTA GACTGTGAAT ATGATGACAC AGATTCTTT TTATGGTGGC TTGCTTGTT 840
TTAAATTTT GCATGACTTT TCATCTTTT ATGATGTTT CCTGTAGTTT GATCCGAAGG 900
AAAAGAGTAT AGTAGCCTGA GAATCAGGAG ATGGGAGTT TAGTCGTAGG CCTTATGATA 960
ATTACCCCGC GGTGGTGTG AGAAAAGTAT GTAAATTGCA TCTGTTTAA GACTTTGAAC 1020
TACCTAAGA AGAGGAATCT AATACAATAT TTGTAATGTT AAAAAAAA AAAAAAAA 1080
AAAAAAAAA
  
```

1088

(2) INFORMATION ON SEQ ID NO. 260:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 3292 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:
- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

ATGCCGAACT TCTGCGCTGC CCCCAACTGC ACGCGGAAGA GCACGCGACT CGACTTGGCC 60
 TTCTTCAGGT TCCCCGGGA CCCTGCCAGA TGCCAGAAGT GGTTGGAGAA CTGTAGGAGA 120
 GCAGACTTAG AAGATAAAAAC ACCTGATCAG CTAATAAAC ATTATCGATT ATGTGCCAAA 180
 CATTTTGAGA CCTCTATGAT CTGTAGAAGT AGTCCTTATA GGACAGTCT TCGAGATAAT 240
 GCAATACCAA CAATATTTGA TCTTACCACT CATTGAACA ACCCACATAG TAGACACAGA 300
 AAAACGAATAA AAGAACTGAG TGAAGATGAA ATCAGGACAC TGAAACAGAA AAAAATTGAT 360
 GAAACTTCTG AGCAGGAACA AAAACATAAA GAAACCAACA ATAGCAATGC TCAGAACCCC 420
 AGCGAAGAAG AGGGTGAAGG GCAAGATGAG GACATTTAC CTCTAACCT TGAAGAGAAG 480
 GAAAACAAAG AATAACCTAAA ATCTCTATT GAAATCTTGA TTCTGATGGG AAAGCAAAAC 540
 ATACCTCTGG ATGGACATGA GGCTGATGAA ATCCCAGAAG GTCTCTTAC TCCAGATAAC 600
 TTTCAGGCAC TGCTGGAGTG TCGGATAAAT TCTGGTGAAG AGGTTCTGAG AAAGCGGTTT 660
 GAGACAACAG CAGTTAACAC GTTGTGTTGT TCAAAACAC AGCAGAGGCA GATGCTAGAG 720
 ATCTGTGAGA GCTGTATTG AGAAGAAACT CTCAGGGAAG TGAGAGACTC ACACCTCTT 780
 TCCATTATCA CTGACGATGT AGTGGACATA GCAGGGGAAG AGCACCTACC TGTGTTGGTG 840
 AGGTTTGTG ATGAATCTCA TAACCTAAGA GAGGAATTAA TAGGCTTCT GCCTTATGAA 900
 GCCGATGCAG AAATTTTGGC TGTGAAATT CACACTATGA TAACTGAGAA GTGGGGATTA 960
 AATATGGAGT ATTGTCGTGG CCAGGCTTAC ATTGTCTCTA GTGGATTTC TTCCAAAATG1020
 AAAGTTGTTG CTTCTAGACT TTAGAGAAA TATCCCAAG CTATCTACAC ACTCTGCTCT1080
 TCCTGTGCT TAAATATGTG GTTGGCAAA TCAGTACCTG TTATGGAGT ATCTGTTGCA1140
 TTAGGAACAA TTGAGGAAGT TTGTTCTTT TTCCATCNGA TCACCCAAAC TGCTTTAGA1200
 ACTTGACAAAC GTAAATTGCTG TTCTTTTCA GAACAGTAAA GAAAGGGTA AAGAACTGAA1260
 GGAAATCTGC CATTCTCAGT GGACAGGGCAG GCATGATGCT TTTGAAATT TAGTGGAACT1320
 CCTGCAAGCA CTTGTTTAT GTTGTAGATGG TATAAATAGT GACACAAATA TTAGNATGGG1380
 AATAACTATA TAGCTGGCCG AGCATTNGT ACTCTGCAGT GCAGTGTCA GATTTGATTT1440
 CATTGTTACT ATTGTTGTTT TTAAAAATGT CCTATCTTT ACAAGAGCCT TTGGGAAAAA1500
 CCTNCANGG GGCAAACCTC GTGATGCTT CTTGCGGCC GGTAGCTGA CTNGCAGTAC1560
 TGNNCATTCA CNTCAACGAA GTGAGTGGGA AAATATTNGA AGTTTATCAT GAATTTGGT1620
 TTGAGGAAGC CACAAATTG GCAACCAAAC TTGATATTCA AATGAAACTC CCTGGGAAAT1680
 TCCGCAGAGC TCACCCNNAGG GTAACTTGGG ATTCAGCTA ACNCTCTGAG AGTTACTATA1740
 AAGAAACCCN TAAGTGTCCC AACAGTGGAG CACATTATTC AGGAACTAA AGATATATTTC1800
 TCAGAACAGC ACCTCAAAGC TCTTAAATGC TTATCTCTGG TACCCCTCAGT CATGGGACAA1860
 CTCAAATCA ATACGNTCNG GAGGAACACC ATGCTGACAT GTATAGAAGT GACTTACCCA1920
 ATCCCTGACAC GCTGTCAGCT GAGCTTCATT GTTGGAGAAT CAAATGGAAA CACAGGGGAA1980
 AAGATATAGA GCTTCGCTCC ACCATCTATG AAGCCCTCCA CCTGCCTGAC ATCAAGTTT2040
 TTCCTAATGT GTATGCTATTG CTGAAGGTCC TGTGTATTCT TCCCTGTGATG AAGGTTGAGA2100
 ATGAGCGGT ACGAAATGGN ACGAAAGCGT CTTAAAGCA TATTGAGGG AACACTTGA2160
 CAGACCCAAA GGTCAAAGTAA CTTGGCTTT GCTTTAACAT AAATTTGGA TATTAACAA2220
 CGACCTGGAT TTAATGGTGG ACACATATAT TAAACTCTAT ACAAGTAAGT CAGAGCTTCC2280
 TACAGATAAT TCCGAAACTG TGGNAAAATA CCTAAGAGAC TTTTAAAT AGGCTTTCTT2340
 ATATTGATA TTTGGAAGAA AAAGCCGAA GGTGTATGTA GACCACTAA TCACAAATA2400
 TCTTGCCCTA TAGGACTCCA TTGAATACAT TAGCCATTGA TAATCTACCT GTTAAATGG2460
 CCCCTGTTG AACTCTCAAG CTTGAAAGAC CTACCTGTT TCCTCAGAAGA GAACGTTGAA2520
 AGTGCCTATGT TTCCNTTTG CGTGTCTCT GTTGTGGCA CTCTGGAATT GTTCAGTTA2580
 AGTCATTAA GACATAGCAT TTATTATCAC TGTGGNATCT CTACTTGTG GGTGTTATGA2640
 ATTCTTGNA AGNAAATATA TTTTNGAAGA GGTGTGGGNA GGNAAGGAAT ACNATTTAT2700
 NAAAATGTT TAGTGNAAGN CCCACAATTN GACCTTNGA CTAATANGGA GTTTAAGTA2760
 TNGTAAAAA TNCTATACTG GNNACAGNTT ACAAGAAATT ACCGGAGAAA AGCTTGTGAG2820
 CTCACCNAAA CAAGGNATT NCAGTGTAGA TTTGTCNTT TCTTGAACNT TNAAAGAAAN2880
 CAAATGANCA AAGTTGAAT NGGAAAGCC TGCTGTTGTT CCNACATCTC NGTTGCTGTT2940
 NNTACANTTC CNNNTTTGTG GAGNCCTACN ATCTTNCCTA AGCTTTTNA GCANGGTATA3000

TNGTTGAACA CTTCTNGTTT CATGGTTGAG ACAGAATCAG AGGCCATGGA TACTGACAAC3060
 TGATTTGTCT GTTTTTTTC TCTGTCTTTN TTCCATGACT CTTATATACT GCCTCATCTT3120
 GATTTATAAG CNAAAANCCT GGAAACCT ANCAAAATAA GTGTTGTGGT TTATCTAGAA3180
 AAATATGGAA AATATTGCTG TTATTTTGG TGAAGAAAAT CNAATTGTG ATAGTTATT3240
 TCAATCTAA TAAAATGTGA ATTTGTGTTT AAAAAAAAAA AAAAAAAAAA AA 3292

(2) INFORMATION ON SEQ ID NO. 261:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1196 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vi) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

GGTAGAAAAT GCAATAAATT CTGGGACAAT GCCCGACACT CTGGCATAGA GGAGCCTTCT 60
 GAGACAAAGG GTTCTATGCA AAAAGCAAAT TTCAAATATA AGTTGGTTCC TGAAGAAGAA 120
 ACCACTGCCT CAGAAAATAC AGAGATAACC TCTGAAAGGC AGAAAGAGGG CATCAAATTA 180
 ACAATCAGGA TATCAAGTCG GAAAAGAAC CCCGATTCTC CCCCCAAAGT TCTAGAACCA 240
 GAAAACAAGC AAGAGAACAG AGAAAAGGAA GAGGAGAAAA CAAATGTGGG TCGTACTTTA 300
 AGAAGATCTC CAAGAATATC TAGACCCACT GCAAAAGTGG CTGAGATCAG AGATCAGAAA 360
 GCTGATAAAA AAAGAGGGGA AGGAGAACAGT GAGGTGGAAG AAGAGTCAC AGCTTGCAA 420
 AAAACTGACA AAAAGGAAAT TTTGAAAAAA TCAGAGAACAG ATACAAATTCAAAAGTAAAGC 480
 AAGGTAAAAC CCAAAGGCAA AGTTCGATGG ACTGGTTCTC GGACACGTGG CAGATGGAAA 540
 TATTCCAGCA ATGATGAAAG TGAAGGGTCT GGCAGTGAAA AATCATCTGC AGCTTCAGAA 600
 GAGGAGGAAG AAAAGGAAAG TGAAGAACCC ATCCTAGCAG ATGATGATGAA ACCATGCAA 660
 AAATGTGGCC TTCCAAACCA TCCTGAGCTA ATTCTCTGT GTGACTCTTG CGATAGTGG 720
 TACCATACTG CCTGCCTTCG CCCTCCTCTG ATGATCATCC CAGATGGAGA ATGGTTCTGC 780
 CCACCTTGCC AACATAAAACT GCTCTGTGAA AAATTAGAGG AACAGTTGCA GGATTGGAT 840
 GTTGCCTTAA AGAAGAAAGA CGGTGCCGAA CGAAGAAAAG AACGCTTGGT GTATGTTGGT 900
 ATCAGTATG AAAACATCAT TCCTCCACAA GAGCCAGACT TTTCTGAAGA TCAAGAAGAA 960
 AAGAAAAAAAG ATTCAAAAAAATC CAAAGAGA AACTTGCTTG AAAGGAGGTC AACAGAACAA 1020
 AGGAAATGTA TAAGCTACAG ATTTGATGAG TTTGATGAAAG CAATTGATGAA AGCTATTGAA 1080
 GATGACATCA AAGAAGCCGA TGGAGGAGGA GTTGGCCGAG GAAAAGATAT CTCCACCATC 1140
 ACAGGTATC GTGGAAAGA CATCTCTACT ATTTTGGATG AAAAAATAAT AACGGC 1196

(2) INFORMATION ON SEQ ID NO. 262:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1467 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

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AAGGACGCTT GCCTTTTC GGTCGGGGAA GGGGGAAGAA GGTAACCTCC GGTGACGGGG 60
TTGCATCACT TCCTCTCAAG CTTGGCGTT TGTGGGTGG GTTACACGC GGGTCACACA 120
TGCATATCGA AAAGTGTAT TTCTGTCGG GCCCCATCTA TCCTGGACAC GGCATGATGT 180
TCGTCCGCAA CGATTGCAAG GTGTTCAAGAT TTGCAAATC TAAATGTCAT AAAAACTTA 240
AAAAGAAGCG CAATCCTCGC AAAGTTAGGT GGACCAAAGC ATTCCGGAAA GCAGCTGGTA 300
AAGAGCTTAC AGTGGATAAT TCATTTGAAT TTGAAAAACG TAGAAATGAA CCTATCAAAT 360
ACCAGCGAGA GCTATGGAAT AAAACTATTG ATGCGATGAA GAGAGTTGAA GAAATCAAAC 420
AGAAGCGCCA AGCTAAATT ATAATGAACA GATTGAAGAA AAATAAAGAG CTACAGAAAG 480
TTCAGGATAT CAAAGAAGTC AAGCAAAACA TCCATCTTAT CCGAGCCCCT CTTGCAGGCA 540
AAGGGAAACA GTTGGAAAGAG AAAATGGTAC AGCAGTTACA AGAGGATGTG GACATGGAAG 600
ATGCTCCTTA AAAATCTCTG TAACCATTTC TTTTATGTAC ATTTGAAAAT GCCCTTTGGA 660
TACTTGGAAC TGCTAAATTAA TTTTATTTT TACATAAGGT CACTTAAATG AAAAGCGATT 720
AAAAGACATC TTCTCTGCAT TGCCATCTAC ATAATATCAG ATATTACGGA TGTAGATTG 780
CATCTCAGTG TAAATCTTT ACTGATAGAT GTACTTAAGT AAATCATGAA AATTCTACTT 840
GTAACTATAG AAGTGAATTG TGGACGTTAA ATGGTTGTGC TATTGATAAT ATGGCACTAG 900
GCAGCATTG TATAGTAACT AATGGCAAAA ATTCACTGGCT AGTGTATGAT AAAATAAAT 960
ATTCTTGCA GTAAAAATATT CCCTTTGTTA ATGTTATAGA AGGGGGATA CAAAAAGGAA1020
CTAACAAATT GTATGGCAGT GTCAGATATT TTATTTTAG TATTCCTGT TTTGGTTTAT1080
TTGCATCTTA GAAGAGCATA ATGACATTGT TTGATGAAGC CTAATTATGC TGGACTGTT1140
TGACCTGGTT TAACCCCTCT GATAGGTAGT TGTTGATGCT GGGGATGAGA ACTGAATAAT1200
CTTGCCTGG AGTGACACTA CACTCTAGAA TTCCACTTT GGAGAATACT CAGTTCCAAC1260
TTGTGATTCC TGATAGAACA GACTTTACTT TTCTAGCCCA GCATTGATCT AGAAGCAGAG1320
GAATCCCAGC GCCTTTAAA AGTTGTTATG TGTTTTCTT TTAAAAAGCT CCTGTTTG1380
GAAAGTAGAA TTATGGGTA CAACGTATGT TCATTATTTG TACATAAAAT AAAACCATT1440
AAAAAGTAAA AAAAAAAA AAAAAAC 1467

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(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 739 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CGGCTCGAGC CCCGCTCACT CACCCGCAGC AGGC GTGCAG TTTCCCGGCT CTCCGCGCGG 60
 CGGGGAAGG TCAGCGCCGT AATGGCGTTC TTGGCGTCGG GACCCTACCT GACCCATCAG120
 CAAAAGGTGT TGCGGCTTTA TAAGCGGGCG CTACGCCACC TCGAGTCGTG GTGCGTCCAG180
 AGAGACAAAT ACCGATACTT TGCTTGTTG ATGAGAGGCC GGTTTGAAGA ACATAAGAAT240
 GAAAAGGATA TGCGGAAGGC CACCCAGCTG CTGAAGGAGG CCGAGGAAGA ATTCTGGTAC300
 CGTCAGCATC CACAGCCATA CATCTTCCCTG GACTCTCCCTG GGGGCACCTC CTATGAGAGA360
 TACGATTGCT ACAAGGTCCC AGAATGGTGC TTAGATGACT GGCATCCTTC TGAGAAGGCA420
 ATGTATCCTG ATTA CTTGC CAAGAGAGA CAGTGGAAAGA AACTGC GGAG GGAAAGCTGG480
 GAACGAGAGG TTAAGCAGCT GCAGGGAGAA ACGCCACCTG GTGGTCCCTT AACTGAAGCT540
 TTGCCCCCTG CCCGAAAGGA AGGTGATTG CCCCCACTGT GGTGGTATAT TGTGACCAGA600
 CCCCAGGAGC GGGCCATGTA GAAAGAGAGA GACCTCATCT TTCATGCTTG CAAGTGAAAT660
 ATGTTACAGA ACATGCACTT GCCCTAATAA AAAATCAGTG AAATGGAAAA AAAAAAAAAA720
 AAAAAAAAAA AAAAAAAAAA

739

(2) INFORMATION ON SEQ ID NO. 264:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2146 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TTTTTTTTTT TTTTTTTTTT TCCCAGGCC CCAAAACCATC 60
 CACTTGAAA TTCTTGGTC TCCCATCAGC TGGAATTAAG TAGGTACTGT GTATCTTGA 120
 GATCATGTAT TTGTCTCCAC CTTGGTGGAT ACAAGAAAGG AAGGCACGAA CAGCTGAAA 180
 AGAAGGGTAT CACACCAGCTC CAGCTGGAAT CCAGCAGGAA CCTCTGAGCA TGCCACAGCT 240
 GAACACTTAA AAGAGGAAAG AAGGCACAGCT GCTCTTCATT TATTTGAAA GCAAATTCA 300
 TTGAAAGTGC ATAAATGGTC ATCATAAGTC AAACGTATCA ATTAGACCTT CAACCTAGGC 360
 TATTTAATAA TACACCACAC TGAAATTATT TGCCAATGAA TCCCCAAAGAT TTGGTACAAA 420
 TAGTACAATT CGTATTGCT TTCTCTTTC CTTTCTTCAG ACAAAACACCA ATAATAATGC 480
 AGGTGAAAGA GATGAACAC GACTAGAGGC TGACTTAGAA ATTTATGCTG ACTCGATCTA 540
 AAAAAAATTA TGTTGGTTAA CGTTAACCTA TCTAAAATCG GGCCCTTCG GCAAGCCTT 600
 CAAAGGAGGT CAAGTCACAG TCATACAGCT AGAAAAGTCC CTGAAAAAAA GAATTGTTAA 660
 GAAGTATAAT AACCTTTCA AAACCCACAA CGCAGCTTAG TTTTCTTTA TTTATTGTTG 720
 GTCATGAAGA CTATCCCCAT TTCTCCATAA AATCCTCCCT CCATACTGCT GCATTATGGC 780
 ACAAAAGACT CTAAGTGC CA CCAGACAGAA GGACCAAGAGT TTCCGATTAT AAACAATGAT 840
 GCTGGGTAAT GTTAAATGA GAACATTGGA TATGGATGGT CAGATGAAAG CTCGAGCCGA 900
 ATTCCGGCTCG AGCTTTCATC TGACCATCCA TATCCAATGT TCTCATTAA ACATTACCA 960
 GCATCATTGT TTATAATCAG AAACCTCTGGT CTTCTGTCT GGTGGCACTT AGAGTCTTT 1020
 GTGCCTATAAAT GCAGCAGTAT GGAGGGAGGA TTTTATGGAG AAATGGGGAT AGTCTTCATG 1080
 ACCACAAATA AATAAAGGAA AACTAAGCTG CATTGTGGGT TTTGAAAAGG TTATTATACT 1140
 TCTTAACAAT TCTTTTTCA GGGACTTTTC TAGCTGTATG ACTGTTACTT AACTATCTA 1200
 AAATAGAGCA TTTTGGTATC TTCATCTGA CCATCCATAT CCAATGTTCT CATTAAACA 1260
 TTACCCAGCA TCATTGTTA TAATCAGAAA CTCTGGTCT TCTGTCGTT GGCACATTAGA 1320
 GTCTTTGTG CCATAATGCA GCAGTATGGA GGGAGGATT TATGGAGAAA TGGGGATAGT 1380
 CTTCATGACC ACAAAATAAT AAAGGAAAAC TAAGCTGCAT TGTGGGTTT GAAAAGGTTA 1440
 TTATACTTCT TAACAATTCT TTTTTTCAGG GACTTTCTA GCTGTATGAC TGTTACTTGA 1500
 CCTTCTTTGA AAAGCATTCC CAAAATGCTC TATTTTAGAT AGATTAACAT TAACCAACAT 1560
 AATTTTTTT AGATCGAGTC AGCATAAATT TCTAAGTCAG CCTCTAGTCG TGGTCATCT 1620
 CTTTCACCTG CATTTTATTG GGTGTTGTC TGAAAGAAAAGG AAAGAGGAAA GCAAATACGA 1680
 ATTGTACTAT TTGTACCAAA TCTTGGGAT TCATTGGCAA ATAATTTCAG TGTGGTGTAT 1740
 TATTTAAATAG AAAAAAAATTTTGGTCTC TAGGTTGAAG GTCTAATTGA TACGTTGAC 1800
 TTATGATGAC CATTATGCA CTTTCAAATG AATTTGCTT CAAAATAAT GAAGAGCAGC 1860
 TGTCTTTCTT TCCTCTTTA AGTGGTCAGC TGTGGCATGC TCAGAGGTTG CTGCTGGATT 1920
 CCAGCTGGAG CGGTGTGATA CCCTCTTT TCAGCTGTC GTGCCTTCCT TTCTTGTATC 1980
 CACCAAAGTG GAGACAAATA CATGATCTA AAGATACACA GTACCTACTT AATTCCAGCT 2040
 GATGGGAGAC CAAAGAATTG GCAAGTGGAT GGTTGGTAT CACTGAAAT AAAAGAGGG 2100
 CCTGGGAATT CTTGCGATTC CATCTCTAAA AAAAAAAA AAAAAA 2146

(2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1020 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

- (vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

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CAAGTAAATG CAGCACTAGT GGGTGGGATT GAGGCTATGC CCTGGTGCAT AAATAGAGAC 60
TCAGCTGTGC TGGCACACTC AGCGGCTCTG GACCGCATCC TAGCCGCCGA CTCACACAAG 120
GCAGGGTGGGT GAGGAATCC AGAGTTGCCA TGGAGAAAAT TCCAGTGTCA GCATTCTTGC 180
TCCTTGTGGC CCTCTCTTAC ACTCTGGCCA GAGATACCAC AGTCAAACCT GGAGCCAAAA 240
AGGACACAAA GGACTCTCGA CCCAAACTGC CCCAGACCCCT CTCCAGAGGT TGGGGTGACC 300
AACTCATCTG GACTCAGACA TATGAAGAACG CTCTATATAA ATCCAAGACCA AGCAACAAAC 360
CCTTGATGAT TATTATCATCAC TTGGATGAGT GCCCACACAG TCAAGCTTTA AAGAAAAGTGT 420
TTGCTGAAAAA TAAAGAACAT CAGAAATTGG CAGAGCAGTT TGTCTCTTC AATCTGGTTT 480
ATGAAACAAAC TGACAAACAC CTTTCTCTG ATGGCCAGTA TGCCCCCAGG ATTATGTTTG 540
TTGACCCATC TCTGACAGTT AGAGCCGATA TCACTGGAAG ATATTCAAAC CGTCTCTATG 600
CTTACGAACC TGCAGATACA GCTCTGTTGC TTGACACAT GAAGAAAGCT CTCAAGTTGC 660
TGAAGACTGA ATTGTAAAGA AAAAAAAATCT CCAAGCCCTT CTGTCTGTCA GGCCTTGAGA 720
CTTGAAACCA GAAGAAGTGT GAGAAGACTG GCTAGTGTGG AAGCATAGTG AACACACTGA 780
TTAGGTTATG GTTTAATGTT ACAACAACTA TTTTTTAAGA AAAACAAAGTT TTAGAAATTT 840
GGTTTCAAGT GTACATGTGT GAAAACAATA TTGTATACTA CCATAGTGAG CCATGATTTT 900
CTAAAAAAAAA AAATAAAATGT TTTGGGGGTG TTCTGTTTC TCCAAAAAAA AAAAAAAA 960
AAAAAAAAAA AAAAAAAA AAAAATTGCC CCCAAGGGGA CGGGTTACAA TTGGGGGGCG1020

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(2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1652 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

AATTCGGATC CATGGGCCAC AGTGGATGGC TTGAAATGTG GCTGAGCGCT TCGGACAATT 60
 CGGATCCATG NNNNGTGGCC ACCCCAAGAC GCGCCCCAGC CCGCCATGGC CCGGATCCTN 120
 NCCGGNNNTC CTGCCTTCTG TCCCTGCTCC TGGCCGGNGT TTGTTCCGCC GGGCCGGGGA 180
 CAAGAGAAAGT CTAAGACAGA CTGCCATGGC GGTNATGAGT GGTACCATCT ACGAGTATGG 240
 AGCCCTCACC ATCGATGGGG AGGAATAACAT TCCTTTAAG CAGTATGCAG GCAAATATAT 300
 CCTCTTGTC AACGTAGCCA GCTACTGAGG TCTGACAGAC CAATACCTG AACTGAATGC 360
 ACTACAAGAA GAACTGGGC CATTGGCTN TGGTCATTCT GGGCTTCCCT TCCAACCAAT 420
 TTGGCAAACA GGAGCCAGGC GAGAACTCGG AGATACTCCC CAGTCTCAAG TATGTTCGNN 480
 ACCAGGTNNG GGGGCTTGT GNCCTAATTN NNNTCCAGNC TCNTTGAGA AANNGGANGA 540
 TNGTNGAACN GGGGAGNAAA GAGCNAGAAA TTCTACACTT TCCTGAAGAA CTCCTGCCCT 600
 CCCACTGCAG NAACCTCTGG GNCTCANCCT GGCGCNCCTC TTTTGGGAAC CCATGAAGAT 660
 CCATGACATN CCGCTGGAAC TTTGAGAAAGT TCCTGGTNNG GGCCNAGANT GGCATACCGG 720
 TTATGCGCTG GTACCACCOG ACCACAGTCN AGCAACGTCN AAGATGGACA TCCTGNTCNT 780
 TACATGAGGC GGCAGGGCANG CCCTGANGCG CCNAGGGGGN AAGTAACCTGA NTGCCNNNC 840
 CACCCCTACCC CTACCCCCCTG CCCATCATNG CAAGGGCCGA NGGAGGGGGCT CTTNCAGGAA 900
 GGAAGGCCACA TTCCCAGTCA TTCTNANCC CCACCCCCAGA TTCTCTTNC TTNATTACAT 960
 AAAAGACAAG CCNTGGCAC AACTGTGTGTC TGAACCACTG TNNGACACGT GACAATTGTN1020
 CCCAGTGTGT GCATGGCTAC ACAGNCCACG TATCTGCCCTG CNTTGAACCC CANGGNATG1080
 GTCCATCNTG TNGTTTACGG NCTTGGCACA ACACCCNNTC ATATTTTTT CAGCNTTCT1140
 GTTCCAAANN TGAGNNCCCA AANNGGAAAC ACNAANGTTC TNAGGTCCNA ATNGGTTCTG1200
 CTCAAANCCN TGANACATNC ATTCTTGGG GNCCANGCAT CNTCCCACAT NGCCCACACN1260
 TACACACCAC CNAGCCTCCT TCTTCTTNC CTGNAAGGAC CCNTCCNNNN TGAGCCCCA1320
 AGCCNCATCC CACAGTGCNT CCTGAGACCA GCCAAGACAA CTGTGAGCGC GATGGCCGTG1380
 TANCCCCAGG TNCAGGGGNT GGTGCTCTA TGAAGGGANNG GGNNCNNCGNA AGCCCTTGTN1440
 GGGNCGGNGC CTCCCCGTGAG CCCNGTCTGT GGTGCCNAGC CCTTAGTGCA TTCAGGCTTA1500
 GGCTCCCNAG GCANGGGACA CTACCCCCGC GCCTCTGGAG GACATGCTAT CCTCTCACTC1560
 TGTCCACTGG TATCTCAACA CCCCCATCTG CCCAGTAAAG GTCTTCTGC AGCAAAAAAA1620
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GG 1652

(2) INFORMATION ON SEQ ID NO. 267:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1409 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

GGAGTGGCCC TCTGTGAGGG GCTCAAATGG TTGCAATTCA TGGCGCGTTA CGACTTGGCT 60
 CACTTAATCA AATCCCTACC AACTCTAACT TGCCCGAAGGA AGAACTTGAC CTCTTGGAGA 120
 ACCCTCGATT GGTTTTCCCT GCCATTTAGA TGTTGAAGTA CCCCCATGAAG AGCTGCAGAA 180
 ATTCTCAAAG GTGGATTACA GGAGGTGGCA GAACAGTTAG AGCTGGAACG GATAGGACCA 240
 CAACATCAGG CAGGATCTGA TTCATTGCTC ACAGGAATGG CCTTTTTCAA AATGAGAGAA 300
 ATGTTCTTG AAGATCATAT TGATGATGCC AAATATTGTG GTCATTGTA TGGCCTTGGT 360
 TCTGGTTCAT CCTATGTACA GAATGGCACCA GGGATGCAT ATGAAGAGGA AGCCAACAAG 420
 CAGTCATGAC ATGAAATAGT CCTTTTATTT TTATTTGAG CTACACACAT GCTGTATAT 480
 AGGTTTTATC TCTGGTTGAA TCCCTCGAAC AATAGACAGT ACCTTTCCCC CCCCTTTCAT 540
 GGCCCATTTC ATTGTCTGCC TTTCAGTACT AAGTATGACC GTTCCTATCT CAGATCTAA 600
 TAAAAAAGAAA AAAAAGACG CATTCAAGGTT AAATTTGGCC TTAATTAAAT ATACTTGTAA 660
 GCAAGCGTGT GTGACAGAGA GTGGGGAAAG CTACATCATT GAATATTGTG ATAAACTTTA 720
 CCGACTTGAG TTTGGTTAT TTTTCCCTTT TCCTAAATTA ACTAGCACTG ACTGTAATT 780

ATTTCCCTGT TTCACCGTCTC TCCCTTCCAT TCTGCAGGAG TTTAGCTAT TTGAGATCGT 840
 GGACCATCAG TTTTGCACCT TAGAGACTGT TTCTGACTCT AAACCTGTT TATCAGAAAA 900
 TTGTTTTTCTT CTTGATCTTA GCTGGAAAAA TCTGCCAACT TTACACAGTA TTACTTGGT 960
 TTGACCCAC AGAATATAGC ACGTTGTGCA AACTGTGAT TCAGCGAAAC TTAAAAAAAGA1020
 CAAGAAACTA CTGAGGAGCT TAGTAACTGC TGTTCTGTA CGTAGTGTGTT AATCTTCAA1080
 GCACATCTAG TGTCTGTCAG TTTCTAATTG GCATGTGTAG GCTGCTCTGT GACTGAAGAA1140
 TTTTCAAACC AGCTTACAC CCTTCAGGAA AAATCCCTGT GATTGGATGG TTACTATCTG1200
 CCAGGAACCTG GTACCCAGAT GTGAAGCACA GTTATTATGA TAGACACTTC CTGAGTGCTA1260
 TTGTATCCAC ACCATTACCT TTTTTTTAA ATTGGAGCCA TCTATGAGCC TGATTGTGGT1320
 CGCAACCATT GTAAAACCCA GAAAGCCTAG GGATGGCCA ATAATTGGGG AAATGGTGCA1380
 GTGCCAAGGA AATGGGATGG CAAAAGAAG 1409

(2) INFORMATION ON SEQ ID NO. 268:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 900 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vi) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

CCACACGCGTC CCGGAAACGG CGGCAGCGGC GACAGGACCG AGGGGCCTTA GTTGGTGGC 60
 AAGTCGGGGA TCCCAGAAAG AGAACGCGTGA CCCGGAAAGCG GAAACGGGTG TCCGTCCCAG120
 CTCCGGCCTG CCAGTGAGCT TCTACCATCA TGGACCTATT GTTCGGGCGC CGGAAGACGC180
 CAGAGGAGCT ACTGCGGCAG AACCAAGAGGG CCCTGAACCG TGCCATGCGG GAGCTGGACC240
 GCGAGCGACA GAAAATAGAG ACCCAGGAGA AGAAAATCAT TGCAGACATT AAGAAGATGG300
 CCAAGCAAGG CCAGATGGAT GCTGTTCGCA TCATGGCAAAGACTTGGTG CGCACCCGGC360
 GCTATGTGCG CAAGTTGTA TTGATGCGGG CCAACATCCA GGCTGTGTCC CTCAAGATCC420
 AGACACTCAA GTCCAACAAC TCGATGGCAC AAGCCATGAA GGGTGTCAACC AAGGCCATGG480
 GCACCATGAA CAGACAGCTG AAGTTGCCCG AGATCCAGAA GATCATGATG GAGTTGAGC540
 GGCAGGCAGA GATCATGGAT ATGAAGGAGG AGATGATGAA TGATGCCATT GATGATCCCA600
 TGGGTGATGA GGAAGATGAA GAGGAGAGTG ATGCTGTGGT GTCCCAAGGTT CTGGATGAGC660
 TGGGACTTAG CCTAACAGAT GAGCTGTCGA ACCTCCCCCTC AACTGGGGGC TCGCTTAGTG720
 TGGCTGCTGG TGGGAAAAAAA GCAGAGGGCCG CAGCCTCAGC CCTAGCTGAT GCTGATGAGC780
 ACCTGGAGGA ACGGCTTAAG AACCTGCGGA GGGACTGAGT GCCCCTGCCA CTCCGAGATA840
 ACCAGTGGAT GCCCAGGATC TTTTACCAACA ACCCCTCTGT AATAAAAGAG ATTTGACACT900

(2) INFORMATION ON SEQ ID NO. 269:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1145 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GGGCCCCGCC	CAGGCGGCTG	CCCGTGACCT	GCCTGGCGC	GGGAACTGA	AAGCCGGAAG	60
GGGCAAGACG	GGTCAGTTC	GTCATGGGC	TGTTGGAAA	GACCCAGGAG	AAGCCGCCA	120
AAGAACTGGT	CAATGAGTGG	TCATTGAAGA	TAAGAAAGGA	AATGAGAGTT	GTTGACAGGC	180
AAATAAGGGA	TATCCAAAGA	GAAGAAGAAA	AAGTGAACG	ATCTGTGAAA	GATGCTGCCA	240
AGAAGGGCCA	GAAGGATGTC	TGCATAGTTC	TGGCCAAGGA	GATGATCAGG	TCAAGGAAGG	300
CTGTGAGCAA	GCTGTATGCA	TCCAAAGCAC	ACATGAACTC	AGTGCTCATG	GGGATGAAGA	360
ACCAGCTCGC	GGTCTTGCAG	GTGGCTGGTT	CCCTGCAGAA	GAGCACAGAA	GTGATGAAGG	420
CCATGCAAAG	TCTTGTGAAG	ATTCCAGAGA	TTCAGGCCAC	CATGAGGGAG	TTGTCCAAAG	480
AAATGATGAA	GGCTGGGATC	ATAGAGGAGA	TGTTAGAGGA	CACTTTGAA	AGCATGGACG	540
ATCAGGAAGA	AATGGAGGAA	GAAGCAGAAA	TGAAATTGA	CAGAATTCTC	TTTGAAATTAA	600
CAGCAGGGGC	CTTGGGCAAA	GCACCCAGTA	AAGTGAATG	TGCCCTTCCA	GAGCCAGAAC	660
CTCCAGGAGC	GATGGCTGCC	TCAGAGGATG	AGGGGGAGGA	GGAAGAGGCT	CTGGAGGCCA	720
TGCAGTCCCC	GCTGGCCACA	CTCCGCAGCT	AGGGGCTGCC	TACCCCGCTG	GGTGTGCACF	780
CACTCCTCTC	AAGAGCTGCC	ATTTTATGTG	TCTCTTGAC	TACACCTCTG	TTGTGAGGAC	840
TACCATTG	GAGAAGGTTG	TGTTTGTCTC	TTTCATTCT	CTGCCAGGT	TTTGGGATCG	900
CAAAGGGATT	GTTCTTATAA	AAGTGGCATA	AATAAATGCA	TCATTTTTAG	GAGTAGAC	960
AGATATATCT	TATTGTGGGG	AGGGGAAAGA	AATCCATCTG	CTCATGAAGC	ACTCTGAAA1020	
ATATAGGTGA	TTGCCTGAAT	GTCGAAGACT	CTACTTTGT	CTATAAAACA	CTATATAAAAT1080	
GAATTTAAT	AAATTTTGC	TTTAGCAGT	GGCCCCATTG	TAGATTGCC	TGTGCAGTAA1140	
					1145	

(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1836 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

GTTGCAGACAT GCAGTGCAGCC GGAGGAACCTG TGCTCTTGA GGCGCAGCCT AGGGGCCCGG 60
 AAGGGAAACT GCGAGGCAGA GGTGACCGGG GACCGAGCAT TTCAGATCTG CTCGGTAGAC 120
 CTGGTGCACC ACCACCATGT TGGCTGCAAG GCTGGTGTGT CTCCGGACAC TACCTTCTAG 180
 GGTTTCCAC CCAGCTTCA CCAAGGCCCTC CCCTGTTGTG AAGAATTCCA TCACGAAGAA 240
 TCAATGGCTG TTAACACCTA GCAGGGAATA TGCCACCAA ACAAGAATTG GGATCCGGCG 300
 TGGGAGAACT GGCCAAGAAC TCAAAGAGGC AGCATTGGAA CCATCGATGG AAAAATATT 360
 TAATATTGAT CAGATGGGAA GATGGTTGTG TGCTGGAGGG GCTGCTGTG GTCTTGGAGC 420
 ATTGTGCTAC TATGGCTTG GACTGTCTAA TGAGATTGGA GCTATTGAAA AGGCTGTAAT 480
 TTGGCCTCAG TATGTCAAGG ATAGAATTCA TTCCACCTAT ATGTACTTAG CAGGGAGTAT 540
 TGGTTTAACA GCTTGTCTG CCATAGCAAT CAGCAGAACG CCTGTTCTA TGAACTTCAT 600
 GATGAGAGGC TCTTGGGTGA CAATTGGTGT GACCTTGCA GCCATGGTTG GAGCTGGAAT 660
 GCTGGTACGA TCAATACCAT ATGACCAGAG CCCAGGCCA AAGCATCTTG CTTGGTTGCT 720
 ACATTCTGGT GTGATGGGTG CAGTGGTGGC TCCTCTGACAA ATATTAGGGG GTCCCTTCT 780
 CATCAGAGCT GCATGGTACA CAGCTGGCAT TGTGGGAGGC CTCTCCACTG TGGCCATGTG 840
 TCGGCCAGT GAAAAGTTTCA TGAACATGGG TGCAACCCCCCTG GGAGTGGGCC TGGGTCTCGT 900
 CTTTGTGTC TCATTGGGAT CTATGTTCT TCCACCTTAC ACCGTGGCTG GTGCCACTCT 960
 TTACTCAGTG GCAATGTACG GTGGATTAGT TCTTTCTCAGC ATGTTCTTC TGTATGATAC1020
 CCAGAAAGTA ATCAAGCGTG CAGAAGTATC ACCAATGTAT GGAGTTCAAA AATATGATCC1080
 CATTAACTCG ATGCTGAGTA TCTACATGGA TACATTAAT ATATTTATGC GAGTGCAAC1140
 TATGCTGGCA ACTGGAGGC ACAGAAAAGAA ATGAAGTGAC TCAGCTCTG GCTTCTCTGC1200
 TACATCAAAT ATCTTGTAA ATGGGGCAGA TATGCATTAA ATAGTTGTA CAAGCAGCTT1260
 TCGTTGAAGT TTAGAAGATA AGAAACATGT CATCATATT AAATGTTCCG GTAATGTGAT1320
 GCCTCAGGTC TGCTTTTT TCTGGAGAAAT AAATGCAGTA ATCCCTCTCCC AAATAAGCAC1380
 ACACATTTC AATTCTCATG TTTGAGTGT TTTAAAATGT TTTGGTGAAT GTGAAAACTA1440
 AAGTTTGTGT CATGAGAATG TAAGTCTTT TTCTACTTTA AAATTTAGTA GGTTCACTGA1500
 GTAACTAAAA TTAGCAAAC CTGTGTTGC ATATTTTTT GGAGTGCAGA ATATTGTAAT1560
 TAATGTCTA AGTGTGTTGG AGCTTTGGTA AAGGGACCAG AGAGAAGGAG TCACCTGCAG1620
 TCTTTGTGTT TTTAAATAC TTAGAACCTA GCACTTGTGT TATTGATTAG TGAGGAGCCA1680
 GTAAGAAACA TCTGGTATT TGGAACAAAG TGGTCATTGG TTACATTCTAT CTGCTGAAC1740
 TAACAAAACG GTTCCATCC TGGAACAGGG CACAGGTGAA TGCATTCTC CTGCGGTTGG1800
 CTCCCCAGTG GCCCGCCTTC CCATATAGGA TGTGGG 1836

(2) INFORMATION ON SEQ ID NO. 271:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1220 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

TGAAGTTCTA AGAGCTTCC AAGTTGGGA AGGTGTCGG GTTTCTCG ATTACTCTC 60
 TGAGCATGAA CGGAAGTCAC CCTTGTCGC TTATCGGGT ATTTTAATGA TAGGTGTCAT 120
 ATATAGGACG GAGTAATCTG TTACATTCT GTTCTTCTG ATGCACTCAC AAGCGGGTAA 180
 CTAGGTGACA AGAAAACAAA GATCTTATTG AAAAGAGGTC TTACAGCAAC CCAACGTCTC 240
 ATCTTCCCCT AGTAAAGATG ACGGCGCCTT GAGGTAAGCT ACAGGCAACA CCACCTCCGC 300
 GTTTCTCTTG CGCCCTGGTC CAAGATGGCG GATGAAGCCA CGCGACGTGT TGTGTCGAG 360
 ATCCC GGTTGC TGAAGACTAA CGCCGGACCC CGAGATCGTG AGTTGTGGGT GCAGCGACTG 420
 AAGGAGGAAT ATCAGTCCCT TATCCGGTAT GTGGAGAACACA ACAAGAACATGC TGACAACGAT 480
 TGGTTCCGAC TGGAGTCCAA CAAGGAAGGA ACTCGGTGGT TTGGAAAATG CTGGTATATC 540
 CATGACCTCC TGAAATATGA GTTGCACATC GAGTTTGACA TTCTATCAC ATATCCTACT 600
 ACTGCCCCAG AAATTGCACT TCTTGAGCTG GATGGAAAGA CAGCAAAGAT GTACAGGGGT 660
 GGCAAATAT GCCTGACGGG TCATTTCAAA CCTTTGTGGG CCAGGAATGT GCCCAAATTT 720
 GGACTAGCTC ATCTCATGGC TCTGGGGCTG GGTCCATGGC TGGCAGTGGA AATCCCTGAT 780
 CTGATTGAGA AGGGCGTCAT CCAACACAAA GAGAAATGCA ACCAATGAAG AATCAAGCCA 840
 CTGAGGCAGG GCAGAGGGAC CTTTGATAGG CTACGATACT ATTTTCTGT GCATCACACT 900
 TAACTCATCT AACTGCTTCC CGGGACACCC TCCACCTCTA GTTGTACTA AGTAGCTGCA 960
 GTAGGCATTG CTGGGGAAAGA AACAAACACA CACCAAACAG TACTGCTACT TAGTTCTAA1020
 GGCTGCACAG GGAAGGGAAA GACTGGGCTT TGGACAATCT AGAGGTAATT TATATCCGCC1080
 CCCAGGTGGA GCAACATGCG ATTCTGGAGG CACGGGGTA ACTGAAAGTG AGTACATATA1140
 GTCTTCTGG TTTCTGGAGA TAACCCATCA ATAAAAGCTG CTTCCTCTGG TAAAAAAAAA1200
 AAAAAAAA AAAAAAAA
 1220

(2) INFORMATION ON SEQ ID NO. 272:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1303 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CGCAGTGCAG AGGGCGTGGGG CTCTCTCCCT GTCAGTCGGC GCCGCGTGC GGCTGGTGGC 60
 TCTGTGGCAG CGGCCGCGGC AGGACTCCGG CACTATGAGC GGCTTCAGCA CCGAGGAGCG 120
 CGCCGCGCCC TTCTCCCTGG AGTACCGAGT CTTCTCAAA AATGAGAAAG GACAATATAT 180
 ATCTCCATT CATGATATTC CAATTATGC AGATAAGGAT GTGTTTCACA TGTTAGTTGA 240
 AGTACCACGC TGGTCTAATG CAAAAATGGA GATTGCTACA AAGGACCCCT TAAACCTAT 300
 TAAACAAGAT GTGAAAAAAAG GAAAACCTCG CTATGTTGCG AATTGTTCC CGTATAAAGG 360
 ATATATCTGG AACTATGGTG CCATCCCTCA GACTGGGAA GACCCAGGGC ACAATGATAA 420
 ACATACTGGC TGTTGTGGTG ACAATGACCC AATTGATGTG TGTGAAATTG GAAGCAAGGT 480
 ATGTGCAAGA GGTGAAATAA TTGGCGTGA AGTTCTAGGC ATATTGGCTA TGATTGACGA 540
 AGGGGAAACC GACTGGAAAG TCATTGCCAT TAATGTTGGAT GATCCTGATG CAGCCAATTA 600
 TAATGATATC AATGATGTCA AACGGCTGAA ACCTGGCTAC TTAGAAGCTA CTGTTGACTG 660
 GTTTAGAAGG TATAAGGTTG CTGATGGAAA ACCAGAAAAT GAGTTTGCCT TTAATGCAGA 720
 ATTTAAAGAT AAGGACTTTG CCATTGATAT TATTAAGAAGC ACTCATGACC ATTGGAAAGC 780
 ATTAGTGAATC AAGAAAACGA ATGGAAAAGG AATCAGTTGC ATGAATACAA CTTTGTCTGA 840
 GAGCCCCCTTC AAGTGTGATC CTGATGCTGC CAGAGCCATT GTGGATGCTT TACCACCACC 900
 CTGTGAATCT GCCTGCACAG TACCAACAGA CGTGGATAAG TGTTCCATC ACCAGAAAAA 960
 CTAATGAGAT TTCTCTGGAA TACAAGCTGA TATTGCTACA TCGTGTTCAT CTGGATGTAT 1020
 TAGAAGTAAA AGTAGTAGCT TTCAAAGCT TAAATTTGT AGAAACTCATC TAACTAAAGT 1080
 AAATTCTGCT GTGACTAATC CAATATACTC AGAATGTTAT CCATCTAAAG CATTTCAT 1140
 ATCTCAACTA AGATAACTT TAGCACATGC TAAATATCA AAGCAGTTGT CATTGGAAG 1200
 TCACTTGTGA ATAGATGTGC AAGGGGAGCA CATATTGGAT GTATATGTTA CCATATGTTA 1260
 GGAAATAAAA TTATTTGCT GAAACTTGGA AAAAAAAAAA AAA 1303

(2) INFORMATION ON SEQ ID NO. 273:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1586 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CGGCTCGAGC GGCTCGAGAT TCGAGGTGTT GGTGGTCTTG GAAGAGCGTC GAGGGGGCCG 60
 TGGACGTGGA ATGGGCCGAG GAGATGGATT TGATTCTCGT GGCAAACGTG AATTGATAG 120
 GCATAGTGGAA AGTGATAGAT CTGGCCTGAA GCACGAGGAC AACAGTGGAG GTAGCGGATC 180
 TCACAACCTGG GGAACGTGCA AAGACGAATT AACAGAGTCC CCCAAATACA TTCAGAAACA 240
 AATATCTTAT AATTACAGTG ACTTGGATCA ATCAAATGTG ACTGAGGAAA CACCTGAAGG 300
 TGAAGAACAT CATCCAGTGG CAGACACTGA AAATAAGGAG AATGAAGTGTG AAGAGGTAAA 360

AGAGGAGGGT CCAAAAGAGA TGACTTTGGA TGAGTGGAAAG GCTATTCAAATAAAGGACCG 420
 GGCAAAAGTA GAATTTAATA TCCGAAAACC AAATGAAGGT GCTGATGGGC AGTGGAAAGAA 480
 GGGATTGTT CTTCATAAAT CAAAGAGTGA AGAGGCTCAT GCTGAAGATT CGGTATGGA 540
 CCATCATTTC CGGAAGCCAG CAAATGAT AACGCTCAT CGTGAGATCA ATTTTGGAGA 600
 CCTTGGCCGC CCAGGACGTG GCGGCAGGGG AGGACGAGGT GGACGTGGGC GTGGTGGCG 660
 CCCAAACCGT GGCAGCAGGA CCGACAAGTC AAGTGCTTCT GCTCCTGATG TGGATGACCC 720
 AGAGGCATTC CGCAGCTCTGG CTTAACGTGA TGCCATAAGA CAACCCCTGGT TCCTTGTGA 780
 ACCCTTCTGT TCAAAGCTTT TGCGATGCTTA AGGATTCCAA ACAGACTAAGA AATTAAAAAA 840
 AAAAGACTG TCATTCATAC CATTACACACC TAAAGACTGA ATTTTATCTG TTTTAAAAAT 900
 GAACCTCTCC CGCTACACAG AAGTAACAAA TATGGTAGTC AGTTTTGTAT TTAGAAATGT 960
 ATTGGTAGCA GGGATGTTT CATAATTTC AGAGATTATG CATTCTTCAT GAATACTTT 1020
 GTATTGCTGC TTGCAAATAT GCATTTCCAA ACTTGAATA TAGGTGTGAA CAGTGTGTAC 1080
 CAGTTAAAG CTTTCACTTC ATTGTGTTT TTTAATTAAG GATTTAGAAG TTCCCCCAAT 1140
 TACAAACTGG TTTAAATAT TGGACATACT GGTTTAATA CCTGCTTGC ATATTCACAC 1200
 ATGGTCAACT GGGACATGTT AAACTTGAT TTGTCAAATT TTATGCTGTG TGGAAATACTA 1260
 ACTATATGTA TTTAACTTA GTTTAAATAT TTTCATTTTT GGGGAAAAAT CTTTTTCAC 1320
 TTCTCATGAT AGCTGTTATA TATATATGCT AAATCTTTAT ATACAGAAAT ATCAGTACTT 1380
 GAACAAATTC AAAGCACATT TGGTTTATTA ACCCGTGGCT GCCCTGGCAT GGGGCCATT 1440
 TGGGGTCCAA ATTATAACTG ATTTACATTT TCAGCGATAT TACTTTTAAA TGCCCTGAGTT 1500
 CCCATTAAATCTAAACTAG ACACCTAATG GGGAAAGTGGT TAACCACAT GTGGTAGCCA 1560
 CCGGCCAG 1568

(2) INFORMATION ON SEQ ID NO. 274:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

KQVKCAKVSY LLFLFQYCAI DSCIKFWNAG SSWLSSVTLW SMSSVSLAS NVGRVRIKSE 60
 GCSTGDKLSL GVPASKATEP ISFRRRSSCS LCCWLSALAS DFFRRSYSGR YSLSYSSAAL 120
 VTCTKSSSNP VPRTAETPTT LSEL 144

(2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Name: 275 Len: 143 Check: 15DA
 MSLVLDEFYS SLRVVGVS A LGTGLDELFV QVTSAEEYE REYRPEYERL KKSLANAESQ 60
 QQREQLERLR KDMGSVALDA GTPKDSLSPV LHPSDLILTR PTLEADS DTD DIDHRVTEES120
 HEEPAFQNF M QESMAQYWKR NNK 143

(2) INFORMATION ON SEQ ID NO. 276:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 181 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

IPNMAAPLGG MFSGQPPGPP QAPPGLPGQA SLLQAAAGAP RPSSSTLVDE LESSFEACFA 60
 SLVSQDYVNG TDQEEIRTGV DQCQKFLDI ARQTECFFLQ KRLQLSVQKP EQVIKEDVSE120
 LRNELQRKDA LVQKHLT KLR HWQQVLEDIN VQHKKPADIP QGSLAYLEQA SANIPAPLKP180
 T 181

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 89 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

NELIIWQRVL PKCQVHRKEC VANLTHQPTH RPTASALCSR WLQRCRDVGR CLLQVGQGAL60
 RSVGGLFVLH VDV LQHLLPM PQLCQVLLD 89

(2) INFORMATION ON SEQ ID NO. 278:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

MPNFCAAPNC TRKSTQSDL A FFRFP RD P AR C Q K W V E N C R R A D L E D K T P D Q L N K H Y R L C A K 60
 H F E T S M I C R T S P Y R T V L R D N A I P T I F D L T S H L N N P H S R H R K R I K E L S E D E I R T L K Q K K I D 120
 E T S E Q E Q K H K E T N N S N A Q N P S E E E G E G Q D E D I L P L T L E E K E N K E Y L K S L F E I L I L M G K Q N 180
 I P L D G H E A D E I P E G L F T P D N F Q A L L E C R I N S G E E V L R K R F E T T A V N T L F C S K T Q Q R Q M L E 240
 I C E S C I R E E T L R E V R D S H F F S I I T D D V V D I A G E E H L P V L V R F V D E S H N L R E E F I G F L P Y E 300
 A D A E I L A V K F H T M I T E K W G L N M E Y C R G Q A Y I V S S G F S S K M K V V A S R L L E K Y P Q A I Y T L C S 360
 S C A L N M W L A K S V P V M G V S V A L G T I E E V C S F F H X I T T A F R T 401

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

M L I S G T L S H G T T Q I Q Y X X E E H H A D M Y R S D L P N P D T L S A E L H C W R I K W K H R G K D I E L P S T I 60
 Y E A L H L P D I K F F P N V Y A L L K V L C I L P V M K V E N E R Y E N G T K A S L K H I 106

(2) INFORMATION ON SEQ ID NO. 280:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 398 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

GRKCNKFWDN AQTSGIEEPS ETKGSMQSK FKYKLVPEEE TTASENTEIT SERQKEGIKL 60
 TIRISSRKKK PDSPPKVLEP ENKQEKETEKE EEEKTNVGRTL RRSPRISRPT AKVAEIRDQK120
 ADKKRGEGED EVEEESTALQ KTDKKEILKK SEKDTNSKVS KVVKPGKVRW TGSRTGRWK180
 YSSNDESEGS GSEKSSAASE EEEEKESEEA ILADDDEPCK KCGLPNHPEL ILLCDSCDSG240
 YHTACLRPPL MIIPDGEWFC PPCQHKLLCE KLEEQLQDLD VALKKKERAEE RRKERLVYVG300
 ISIENIIPPQ EPDFSEDQEE KKKDSKKSKA NLLERRSTRT RKCISYRFDE FDEAIDEAIE360
 DDIKEADGGG VGRGKDISTI TGHRGKDIST ILDEKIIT 398

(2) INFORMATION ON SEQ ID NO. 281:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 198 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

SSEKSGSCGG MMFSILIPTY TKRSFLRSAR SFFFKATSKS CNCSSNFSQS SLCWQGGQNH 60
 PSPGMIIRGG RRQAVWYPLS QESHRRISSG WFGRPHFLHG SSSSARMASS LSFSSSSSEA120
 ADDFSLPDPS LSSLLEYFHL PRVREPVHRT LPLGFTLLTL EFVSFSDFFK ISFLSVFCKA180
 VDSSSTSSSP SPLFLSAF 198

(2) INFORMATION ON SEQ ID NO. 282:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 202 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

GRLPFSGRGR GKKVTSGDGV ASLPLKLGRL FGGVTRGFNM RIEKCYFCGPIYPGHGMMF 60
 VRNDCKVFRF CKSKCHKNFK KKRNPRAKVRW TKAFRKAAGK ELTVDNSFEP EKRRNEPIKY120
 QRELWNKTID AMKRVEEIKQ KROAKFIMNR LKKNKELOQKV QDIKEVKQNI HLIRAPLAGK180
 GKQLEEKMVQ QLQEDVDMED AP 202

(2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

IICHCKLFTSC FPECFGPPNF ARIALLFKVF MTFRFAKSEH LAIVADEHHA VSRIDGPRTE60
 ITLFDTTHVEP ACNPTKQTPK LERK 84

(2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

RLEPRSVTRS RRAVSRLSAR PGKVASVMAF LASGPYLTHQ QKVLRLYKRA LRHLESWCVQ 60
 RDKYRYFACL MRARFEHKN EKDMAKATQL LKEAEEFWY RQHPQPYIFP DSPGGTSYER120
 YDCYKVPFWC LDDWHPSEKA MYPDYFAKRE QWKKLRESW EREVKQLQEE TPPGGPLTEA180
 LPPARKEGDL PPLWWYIVTR PRERPM 206

(2) INFORMATION ON SEQ ID NO. 285:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 139 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

PLVPSFPSAV SSVLWSQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRCMAV 60
 DADGTRILPR PPSAAGWPSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVAPAYKAA120
 TPFADGSGRV PTPRTPLRR 139

(2) INFORMATION ON SEQ ID NO. 286:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SSWSGVIPFF FSCSCLPFLY60
 PPRWRQIHDL KDTQYLLNSS 80

(2) INFORMATION ON SEQ ID NO. 287:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SSWSGVIPFF FSCSCLPFLY60
 PPKWRQIHD L KDTQYLLNSS 80

(2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

RLSCAGTLSG SGPHPSRRLT QGRWVRKSRV AMEKIPVSAF LLLVALSYTL ARDTTVKPGA 60
 KKDTKDSRKP LPOTLSRGWG DQLIWTQTYE EALYKSCTSN KPLMIIHLD ECPHSQALKK120
 VFAENKEIQK LAEQFVLLNL VYETTDKHL PDGQYVPRIM FVDPSLTVA DITGRYSNRL180
 YAYEPADTAL LLDNMKKALK LLKTEL 206

(2) INFORMATION ON SEQ ID NO. 289:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GNPELPWRKF QCQHSCSLWP SPTLWPEIPQ SNLEPKRTQR TLDPNCPRSS PEVGVTNSSG60
 LRHMKKLYIN PRQATNP 77

(2) INFORMATION ON SEQ ID NO. 290:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 160 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGXGXQLLXP XAXQGXPAAS CXXQDVHLXR CXTVVRWYQR ITGMPXXAPT RNFSKFQRXV 60
MDLHGFPKEX GQXEXQEXLQ WEGRSSSGKC RISXSXLPSX TIXXFLKXXW XXIRXQSPXT120
WXRTYLRLGS ISEFSPGSCL PNWLEGKPRM TXAKWPKFEL 160

(2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 150 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

RHXPLXLGXH GHRAHSCLGW SQXALwdxAW GLXXXGSXQX RKKEAXWCvx VGXVGXCXXP 60
XEXMXXGFEQ NXXGPXNXXV SXLGXXXWNR XAEKNMXGCC AKXVNXXMDH XXGFQXRQIR120
GLCSHAHTGX NCHVSXSGSD TQLCXGLSFM 150

(2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 86 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

RAAKILKGGGL QEVAEQLELE RIGPQHQAGS DSLLTGMAFF KMREMFFEDH IDDAKYCGHL60
YGLGSGSSYV QNGTGNAYEE EANKQS 86

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 64 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

IKAKFNLNAF FFFFFLRLSEI GTVILSTERQ TIKWAMKGGG KVLSIVRGIQ PEIKPIYKHV60
CSSK 64

(2) INFORMATION ON SEQ ID NO. 294:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 226 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

ASTIMDLLFG RRKTPEELLR QNQRALNRAM RELDRERQKL ETQEKKIIAD IKKMAKQGQM 60
DAVRIMAKDL VRTRRYVRKF VLMRANIQAV SLKIQTALKSN NSMAQAMKGV TKAMGTMNRQ120
LKLPQIQKIM MEFERQAEIM DMKEEMMNDA IDDPMGDEED EEEESDAVVVSQ VLDELGSLST180
DELSNLPSTG GSLSVAAGGK KAEAAASALA DADADLEERL KNLRRD 226

(2) INFORMATION ON SEQ ID NO. 295:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

KILGIHWLSR SGRGTQSLRR FLSRSSRSAS ASARAEAAAS AFFPPAATLS EPPVEGRFDS 60
 SSVRLSPSSS RTWDTTASLS SSSSSSPMGS SMASFIISSF ISMISACRSN SIMIFWIWGN120
 FSCLFMVPMA LVTPFMACAI ELLDLSVWIL RDTAWMLARI NTNLR 166

(2) INFORMATION ON SEQ ID NO. 296:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 233 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

KPEGARRVQF VMGLFGKTQE KPPKELVNEW SLKIRKEMRV VDRQIRDQQR EEEKVKR SVK 60
 DAAKKGQKD V CIVLAKEMIR SRKAVSKLYA SKAHMNSVLM GMKNQLAVLR VAGSLQKSTE120
 VMKAMQSLVK IPEIQATMRE LSKEMMKAGI IEEMLEDTFE SMDDQEEMEE EAEMEIDRIL180
 FEITAGALGK APSKVTDALP EPEPPGAMAA SEDEGEAAA LEAMQSRLAT LRS 233

(2) INFORMATION ON SEQ ID NO. 297:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

LMPFQSQNLQ ERWLPORMRG RRKRLWRPCS PGWPHSAARG CLPRWVCTHS SQELPFYVSL 60
 ALHLCEDYH FGEGSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRSIDRY ILLWGGERNP120
 SAHEALLKI 129

(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 351 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TWCCTTMLAA RLVCLRTLPS RVFHFAFTKA SPVVKNNSITK NQWLTPSRE YATKTRIGIR 60
 RGRTGQELKE AALEPSMEKI FKIDQMGRWF VAGGAAVGLG ALCYYGLGLS NEIGAIKEKAV120
 IWPQYVKDRI HSTYMYLAGS IGLTALSAIA ISRTPVLMNF MMRGSWVTIG VTFAAMVGAG180
 MLVRSIPYDQ SPGPKHAWL LHSVGVMGAVV APLTIILGGPL LIRAAWYTAG IVGGLSTVAM240
 CAPSEKFLNM GAPLGVGGL VFVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFSMFLLYD300
 TQKVIKRAEV SPMYGVQKYD PINSMLSIYM DTLNIFMRVA TMLATGGNRK K 351

(2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

RVAPATVVGG RNIDPNEDTK TRPRPTPRGA PMFRNFSLGA HMATVERPPT MPAVYHAALM 60
 RRGPPNIVRG ATTAPITPEC SNOARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120
 MKFMRTGVLL IAMADKAVKP ILPAKYI 147

(2) INFORMATION ON SEQ ID NO. 300:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 188 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

RRLEVSYRQH HFRVSLAPWS KMADEATRRV VSEIPVULKTN AGPRDRELWV QRLKEEYQSL 60
 IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLKYE FDIEFDIPIT YPTTAPEIAV120
 PELDGKTAKM YRGGKICLTD HFKPLWARNV PKFGLAHLMA LGLGPWLAVE IPDLIQKGVI180
 QHKEKCNQ 188

(2) INFORMATION ON SEQ ID NO. 301:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 172 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

SKFGHIPGPQ RFEMIRQAYF ATPVHLCCLS IQLRNCNFWG SSRICDRNVK LDVKLIFQEV 60
 MDIPAFSKPP SSFLVGLQSE PIVVSILVVL HIPDKGLIFL LQSLHPQLTI SGSGVSLQHR120
 DLRHNTSRGF IRHLGPGRKR NAEVVLPVAY LKAPSSLIWE DETLGCKTS FE 172

(2) INFORMATION ON SEQ ID NO. 302:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 320 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

AVRRRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60
 SPFHDIPYA DKDVFHMVVE VPRWSNAKME IATKDPLNPI KQDVKKGKL R YVANLFPYKG120
 YIWNYGAIPQ TWEDPGHNDK HTGCCGDNDP IDVCEIGSKV CARGEIIGVK VLGILAMIDE180
 GETDWKVIAI NVDDPPDAANY NDINDVKRLK PGYLEATVDW FRRYKVPDGK PENEFAFNAE240
 FKDKDFAIDI IKSTHDHWKA LVTKKTNGKG ISCMNTTLSE SPFKCDPDAA RAIVDALPPP300
 CESACTVPTD VDKWFHHQKN

320

(2) INFORMATION ON SEQ ID NO. 303:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 85 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

RVLCSNLHFC IRPAWYFNHY VKHILICINW NIMKWRYILS FLIFEEDSVL QGEGRGALLG60
 AEAAGHSAGVL PPPLPQSHQP ARGAD

85

(2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 247 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSGLK HEDKRGGSGS 60
 HNWGTVKDEL TESPKYIQQO ISYNYSLDLQ SNVTEETPEG EEEHPVADTE NKENEVEEVK120
 EEGPKEMTLD EWKAIQNQKDR AKVEFNIRKP NEGADGQWKK GFVLHKSKE EAHAEDSVMD180
 HHFRKPANDI TSQLEINFQD LGRPGRRGGR GRGGRGRGGR PNRGSRTDKS SASAPDVDDP240
 EAFFPALA

247

(2) INFORMATION ON SEQ ID NO. 305:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

SFGILKHAKA LNRRVHKGTR VVLWHPVKPE LGMPLGHPHQ EQKHLTCRSC CHGLGAHHAH60
 VHLVLPQRHV LGGQGLQN

78

(2) INFORMATION ON SEQ ID NO. 306:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 293 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ATRGAEQDG ASAARPRRW AGGLLQRAAP CSLLPRLRTW TSSSNRSRED SWLKSLFVRK 60
VDPRKDAHSN LLAKKETSNL YKLQFHNVKP ECLEAYNKIC QEVLPKIHED KHYPCTLVGT120
WNTWYGEQDQ AVHLWRYEGG YPALTEVMNK LRENKEFLEF RKARSDMLLS RKNQLLLEFS180
FWNEPVPRSG PNIYELRSYQ LRP GTMIEWG NYWARAIRFR QDGNEAVGGF FSQIGQLYMV240
HHLWAYRDLQ TREDIRNAAW HHKGWEELVY YTVP LIQEME SRIMIPLKTS PLQ 293

(2) INFORMATION ON SEQ ID NO. 307:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 208 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

AHRNSTALLE GRGLQWDHDS GFHFLNKWNC VIYQFLPAMF VPCCIPYVFP GLKIPVSPKM 60
VHHVQLPNLR EESSDGFVTI LSEADCTSPV IAPFNHGWS ELVRPEFIYI RSGSWHRLIP120
ETELQQELIL PGEKHVTSCl TKFQKFLIFS EFIHDFCEGW IASFIPPEVD SLVLLAIPRV180
PSPHQSTRVV FIFVNWLWQHL LTNFVVCF 208